## Delaval, Jan

From:

Sent:

Huynh, Phuong N. Monday, September 09, 2002 1:11 PM Delaval, Jan RE: 09/811,367

To: Subject:

Jan,

Please search polypeptide of SEQ ID NO: 1 against commercial and interference databases.

Thanks, Neon Art unit 1644 Mail 9E12 Tel 308-4844

> Jan Delaval Reference Librarian 3iotechnology & Chemical Library CM1 1E07 – 703-308-4498 jan.delaval@uspto.gov

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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            protein search, using sw model
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2: pir2:*
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asialoglycoprotein C type lectin, B 1 asialoglycoprotein lectin M-ASGP-BP pr-cell surface gly T-cell surface gly NKR-Pl protein hom hepatic lectin - r hepatic lectin B1 natural killer cel phospholipase A(2) hepatic lectin hom Ly-49D-GE antigen natural killer cel natural killer cel NKR-Pl protein hom
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326 2
550 2

## ALIGNMENTS

RESULT 2 138700 NNKR-Pla protein - human C;Species: Homo sapiens (man) C;Accies: Homo sapiens (man) C;Accession: I38700 R;Lanier, L.L.; Chang, C.; Phillips, J.H. J. Immunol. 153, 2417-2428, 1994 A;Title: Human NKR-PlA: A disulfide-linked homodimer of the C-type lectin superfamily A;Reference number: I38700; MUID:94358407 A;Accession: I38700 A;Status: preliminary; translated from GB/EMBL/DDBJ	QY 121 LLQVFLSEAFCWIGLRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPL 180       ::	Query Match  S1.4%; Score 525.5; DB 2; Length 188;  Best Local Similarity 53.5%; Pred. No. 4.6e-42;  Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;  QY 1 MTDSVIYSMLELPTATQAQNDYGPQQKSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWIL 60	RESULT 1  IF9421  mast cell function associated antigen - rat  C;Species: Rattus norvegicus (Norway rat) C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999 C;Accession: I59421 R;Guthmann, M.D.; Tal, M.; Pecht, I. Proc. Natl. Acad. Sci. U.S.A. 92, 9397-9401, 1995 A;Title: A secretion inhibitory signal transduction molecule on mast cells is another A;Reference number: I59421; MUID:96016176 A;Accession: I59421 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-188 <res> A;Cross-references: EMBL:X79812; NID:g1020141; PIDN:CAA56208.1; PID:g1020142 C;Genetics: mafa</res>

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RESULT
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A; Residues: 1-225 <RES>
A; Cross references: EMBL:U11276; NID:g538270; PIDN:AAA21605.1; PID:g544496
C; Superfamily: natural killer cell receptor P1; C-type lectin homology
F;94-210/Domain: C-type lectin homology <LCH>
natural killer cell receptor P1 - N;Alternate names: NKR-P1 protein C;Species: Mus musculus (house mo
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C;Superfamily: C-type lectin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene 17.5 protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: I50146
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                                                                                                                                                                                                                                                                                              SPRPPFSHVCPNAWVGFQGKCYYFSDTESDWNSSREHCHRLGASLATLDTKEEMEFMLQY 179
                                                                                                                                                                                                                                                                                                                                    ASCPS----CPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVF 125
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58; Conserv
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    (house mouse)
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26.6%;
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Pred. No. 1.1e-10;
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Pred. No. 1.7e-11;
6; Mismatches 81
                                          mouse
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C;Species: Homo sapiens (man)
C;Date: 31-Mar:1992 #sequence_revision 31-Mar:1992 #text_change 05-May-2000
C;Accession: PT0372; PT0373
R;Houchins, J.P.; Yabe, T.; McSherry, C.; Bach, F.H.
J. Exp. Med. 173, 1017-1020, 1991
A;Title: DNA sequence analysis of NKG2, a family of related cDNA clones enc.
A;Reference number: PT0372; MUID:91178434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule Type: DNA
A;Residues: I-109, 'H',111-181, 'D',183-227 <GIZ>
A;Cross references: GB:X64716; NID:953395; PIDN:CAA45971.1; PID:9817989
A;Cross references: GB:X64716; NID:953395; PIDN:CAA45971.1; PID:9817989
A;Experimental source: BALB/c 3T3 fibroblastoid cell line
A;Note: sequence extracted from NCBI backbone (NCBIN:113037, NCBIN:113063, NCBIN:113064; NCBIN:113064, M.M.; Ryan, J.C.; Hunter, J.J.; Smith, H.R.; Stark, M.; Seaman, W.E.
J. Immunol. 147, 3229-3236, 1991
A;Title: CDNA cloning of mouse NKR-P1 and genetic linkage with LY-49. Identification A;Reference number: A46456; MUID:92013158
A;Accession: A46456
                                                             A;Cross-references: EMBL;X54867; NID:g35056; A;Experimental source: natural killer cell A;Accession: PT0373
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A; Residues: 1-38, 'L', 40-227 < YOK>
A; Residues: 1-38, 'L', 40-227 < YOK>
A; Cross-references: GB:M77753; NID:g198569; PIDN:AAA39366.1; PID:g198570
A; Note: sequence extracted from NCBI backbone (NCBIN:60429, NCBIP:60431)
C; Superfamily: natural killer cell receptor P1; C-type lectin homology
F; 94-210/Domain: C-type lectin homology < LCH>
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A;Title: A family of genes selectively coexpressed A;Reference number: A46467; MUID:91349596
A;Accession: A46467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N;Contains: natural killer cell receptor group 2, splice form C;Species: Homo sapiens (man)
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A;Accession: A46502
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A; Cross-references: GB:M77676; NID:g20005
A; Experimental source: A-LAK cells, C57BL
                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-233 <HOU1>
                                                                                                                                                                                                                                      A; Accession: PT0372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Note: sequence extracted from NCBI backbone (NCBIN:52378, NCBIP:52379); the sequence R;Giorda, R.; Weisberg, E.P.; Ip, T.K.; Trucco, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N; Alternate names: NKG2-A; NKG2-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         natural killer cell receptor group 2, splice form A
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Residues: 1-95,114-233 <HOU2>
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 IGLR---NNSGWRWEDGSPLNFS--RISSNSFVQTCGAINKNGLQASSCEVPLHGVCKK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAF--CW 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IGLRYTLPDMNWKWINGSTLNSDVLKITGDTENDSCAAISGDKVTFESCNSDNRWICQK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRSHRSALKLSCAGLILLVVTLIGMSVLVRVLIQKPSIEKCYVLIQENLNKTTDCSAKLE 93
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Pred. No. 1.5e-10;
3; Mismatches 71
                                                                                                                                         PIDN:CAA38649.1; PID:g35057
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A; Experimental source: natural ki
C; Genetics:
A; Genetics:
A; Gene: GDB: KLRC2; NKG2-C
A; Cross-references: GDB; 9787095
A; Cross-references: GDB; 12p13
C; Superfamily: natural killer cel
C; Keywords: 91ycoprotein; transmembrane #st
F; 71-96/Domain: transmembrane #st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 natural killer cell receptor group 2-C, splice form 1 - N;Alternate names: NKG-C C:Species: Homo sapiens (man) C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text C;Accession: PT0374
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C:Superfamily: natural killer cell receptor P1; C-type lectin C:Superfamily: natural killer cell receptor P1; C-type lectin C:Keywords: alternative splicing; glycoprotein; transmembrane F:71-9B/Domain: transmembrane #status predicted <TRA>
F:119-229/Domain: C-type lectin homology <LCH>
F:102,103,151,180/Binding site: carbohydrate (Asn) (covalent)
F:119-130,147-229,208-221/Disulfide bonds: #status predicted
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A; Residues: 1-231 <HOU>
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J. Exp. Med. 173, 1017–1020, 1991
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A;Experimental source: natural killer cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: GDB: KLRC1; NKG2
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                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 47; Conserv
                                                                                                                                                                                                                                                                                              Superfamily: natural killer cell receptor P1; C-type lectin homolog; Keywords: glycoprotein; transmembrane protein; 71-96/Domain: transmembrane #status predicted <TRA>; 71-96/Domain: transmembrane #status predicted <TRA>; 27,100,149,178/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Species: Homo sapiens (man)
Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 19-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-references: EMBL:X54869; NID:g35060; PIDN:CAA38651.1; PID:g35061
Experimental source: natural killer cell
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                          ITYSNSCYYIGKERRTWEESLLACTSKNSSLLSIDNEEEIKFLASILPSS--WIGVFRNS
                                                               MKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCWIGL-RNN 138
                                                                                                                                                  POOKSSSKPSCSCLVAITLGLLTAVLLSVLLYQWILCOGSNYST----CASCPSCPDRW 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VNRLKSAQCGSSIIYHCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSIDNEEEMKFLSIISPSS--WIGVFRNSSHHPWVTMNGLAFKHEIKDSDNAELNCAVLQ 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STLIQRHNNSSLNTRTQKARHCGHCPEEWITYSNSCYYIGKERRTWEESLLACTSKNSSL 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WILCOGSNYST-----CASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHL 110
                                                                                                           PPEKLTAEVLGIICIV-----LMATVLKTIVLIPFLEQNNSSPNTRTQKARHCGHCPEEW 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITYAELNLQKASQ----DFQGNDKTYHCKDLPSAPEKLIVGILGIICLILMASVVTIVVIP 94
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27.8%;
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Pred. No. 1.9e
35; Mismatches
                                                                                                                                                                                                                  Score 182; DB 2; Pred. No. 1.1e-09;
                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      family of related cDNA clones
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.9e-10;
                                                                                                                                                                                                                                   Length 231
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                                                                                                                                                    Local
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    MKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDN-QEMSLLQVFLSEAFCWIGL-RN 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SHHPWVTINGLAFKHKIKDSDNAELNCAVLQVNRLKSAQCGSSMIYHCK
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A; Map position: 12p13-12p13
C; Superfamily: natural killer cell receptor P1; C-type lectin
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A;Experimental source: natural killer cell
A;Note: translation of nucleotide sequence is not complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Houchins, J.P.; Yabe, T.; McSherry, C.; Bach, F.H.
J. Exp. Med. 173, 1017-1020, 1991
A;Title: DNA sequence analysis of NKG2, a family of related cDNA clones encoding type A;Reference number: PT0372; MUID:91178434
A;Accession: PT0375
                                                                                                                                                                                                                                                                                                                                                                          A; Gene: GDB:KLRC2; NKG2-C
                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-240 <RES>
A; Cross-references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Natural killer lectin-like receptors have divergent carboxy-termini, A;Reference number: I54524; MUID:94102823
A;Accession: I54524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Adamkiewicz, T.V.; McSherry, C.; Bach, F.H.; Immunogenetics 39, 218, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  natural killer cell receptor group 2-C, splice form 2 - human
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N;Alternate names: integral membrane protein NKG2-D C;Species: Homo sapiens (man) C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-May-2000 C;Accession: PT0375; S15671; S19110
                                                                                                                                                                                                                                                                                                                                          A; Cross-references: GDB:9787095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-216 <HOU>
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 FFDESKNWYESQASCMSQNASLLKVYSKEDQDLLK--LVKSYHWMGLVHIPTNGSWQWED 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37 CLVAITLG------LLTAVLLSVLLYQWILCQGSNYSTCASCPSCPDRWMKYGNHCYY 88
                                                       PQQKSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWILCQGSNYST----CASCPSCPDRW 79
PPEKLTAEVLGIICIV-----LMATVLKTIVLIPFLEQNNSSPNTRTQKARPCGHCPEEW 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CFIAVAMGIRFIIMVAIWSAVFLNSLFNQEVQIP----LTESYCGPCPKNWICYKNNCYQ 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSILSPNLLTIIEMQKGDCALYASSFKGYIENCSTPN 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FSVEEXDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCWIGL---RNNSGWRWED 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42;
                                                                                                                 Ch 17.4%; Score 178.5; DB 2; Similarity 28.6%; Pred. No. 2.4e-09; 46; Conservative 30; Mismatches 70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     GB:L14542; NID:g292360; PIDN:AAA16833.1; PID:g292361
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Pred. No. 1.5e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSNSFVQTCGAIN 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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211

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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-223 <GIO>
A;Residues: 1-223 <GIO>
A;Cross-references: GB:M62891; NID:g205722; PIDN:AAA41710.1; PID:g205723
C;Superfamily: natural killer cell receptor PI; C-type lectin homology
C;Keywords: transmembrane protein
F;94-210/Domain: C-type lectin homology <LCH>
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A; Note: sequence extracted from NCBI backbone (NCBIN:113134, NCBIP:113135)
C; Superfamily: C-type lectin homology
F; 256-377/Domain: C-type lectin homology <LCH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Giorda, R.; Rudert, W.A.; Vavassori, C.; Chambers, W.H.; Hiserodt, J.C.; Science 249, 1298-1300, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: A35917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Rattus norvegicus (Norway rat)
C;Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 24-Sep-1999
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A;Molecule type: nucleic acid
A;Residues: 1-404 <CUR>
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A;Tille: Sequence and expression of a membrane-associated
A;Reference number: A46274; MUID:92390446
A;Accession: A46274
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Proc. Natl. Acad. Sci. U.S.A. 89, 8356-8360, 1992
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Best Local
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                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         373 KFWICKK 379
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       ~ 35
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                                                                          24
                         PRSHRLALKLSCAGLILLVLALVGMSILVRVLVQKPSVEPCRVLIQ-ENLSKTGS-PAKL 92
                                                                          PQQKSSSSKPSCSCLVAITLGLL-TAVLLSVLLYQ-----WILCQGSNYSTCASCPS-- 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LHGVCKK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FTWMGLSDLNQEGTWQWVDGSPLLPSFKQYWNRGEPNNVGEEDCAEFSGNGWNDDKCNLA 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FCWIGLR--NNSG-WRWEDGSPL--NFSRI-----SSNSFVQTCGAINKNGLQASSCEVP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSHHPWVTINGLAFKHEIKDSDHAERNCAMLHVRGLISDQC 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity 39; Conserv
                                                                                                                           l Similarity
49; Conser
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27.1%;
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                                                                                                                      Score 175.5;
Pred. No. 4.2e
14; Mismatches
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Pred. No. 6.9e-09;
23; Mismatches 53;
                                                                                                                                                                         DB 2;
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                                                                                                                                                                         Length
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A; Residues: 102-120;137,'X',139-151 <ODA>
A; Residues: 102-120;137,'X',139-151 <ODA>
C; Superfamily: hepatic lectin; C-type lectin homology
C; Superfamily: hepatic lectin; macrophage: transmembrane protein
E; 36-61/Domain: transmembrane #status predicted <TRA>
E; 173-296/Domain: C-type lectin homology <LCH>
E; 74,186/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:S36676; NID:g249360; PIDN:AAB22171.1; PID:g249361 R;Oda, S.; Sato, M.; Toyoshima, S.; Osawa, T.
J. Biochem. 104, 600-605, 1988 A;Title: Purification and characterization of a lectin-like molecule specific A;Reference number: PX0009; MUID:89197865 A;Accession: PX0009
                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change
C;Accession: JH082; I56167; S60753
R;Lopez-Cabrera, M.; Santis, A.G.; Fernandez-Ruiz, E.; Blacher,
J. Exp. Med. 178, 537-547, 1993
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                                                                     A; Reference number: JH0822; MUID:93340630 A; Accession: JH0822
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A; Residues: 1-304 <SAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Sato, M.; Kawakami, K.; Osawa, T.; Toyoshima, J. Biochem. 111, 331-336, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JX0209
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                       A; Molecule type: mRNA
A; Residues: 1-199 <LOP>
                                                                                                                                                  A; Title: Molecular cloning,
                                                                                                                                                                                                                                                                                               lymphocyte early activation antigen AIM/CD69 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: JX0209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
A;Cross-references: GB:222576; NID:g397938; PIDN:CAA80298.1; PID:g397939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118
                                                                                                                                                                                                                                                                                                                                                                                                                             276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 LTCQLANLKNNGSEVACCPLHWTEHEGSCYWFSESEKSWPEADKYCRLENSHLVVVNSLE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212 K 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186 K 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 ILCQGSNYSTCAS-CPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMSLLQVFLSEAFCWIGLRNNSG-WRWEDGSPL----NFSRISSNSFV-----QTCG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AINKNG-LQASSCEVPLHGVCK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    {\tt KCPKDWLSHRDKCFHVSQTSITWKESLADCGGKGATLLLVQDQEELRFLRNLTKRISSSF}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EQNFLQNRLANVVSWIGLTDQNGPWRWVDGTDFEKGFKNWAPLQPDNWFGHGLGGGEDCA 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -CPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVF---LSEAF 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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27.5%;
                                                                                                                                                  expression, and
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                                                                                                                                                                                                     R.; Esch, F.; Sanchez
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Gaps

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of the human

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A; Note: the the line way.

R; Hamann, J; Fiebig, H; Straus.

J: Immunol. 150, 4920-4927, 1993

A; Title: Expression cloning of the early activation ant A; Reference number: 156167; MUID:93267093

A; Accession: 156167

A; Status: translated from GB/EMBL/DDBJ

A; Molecule type: mRNA

A; Residues: 1-199 < RES>

A; Residues: 1-199 < RES>

Chrera, M.; Hamann, J.; Straus
C; Genetics:
A; Gene: llir
A; Map position:
F; 45-69/Domain:
                                                                                                             C; Accession: JC7608
C; Accession: JC7608
R; Bluang, X.; Yuan, Z.; Chen, G.; Zhang, M.; Zhang, W.; Yu, Y.; Cao, Biochem. Biophys. Res. Commun. 281, 131-140, 2001
A; Title: Cloning and characterization of a novel ITIM containing lec A; Reference number: JC7608; MUID:21092797; pMID:11178971
A; Contents: Dendritic cells
A; Accession: JC7608
A; Molecule type: mRNA
A; Residues: 1-37 < HUAN-
A; Residues: 1-37 <
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A;Cross-references: GDB:132925; OMIM:107273
A;Map position: 12p13-12p12
C;Superfamily: C-type lectin homology
C;Keywords: glycoprotein; phosphoprotein; receptor; transmembrane
F;39-64/Domain: transmembrane #status predicted <TMM>
F;85-194/Domain: C-type lectin homology <LCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      type II lectin-like immunoreceptor - human
C; Species: Homo sapiens (man)
C; Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
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F;18,30/Binding site: phosphate (Ser) (covalent) (by protein kinase
F;31/Binding site: phosphate (Thr) (covalent) (by casein kinase II)
F;166/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:L07555; NID:g291897; PIDN:AAB46359.1; PID:g291898 R;Santis, A.G.; Lopez-Cabrera, M.; Hamann, J.; Strauss, M.; Sanchez-Madrid, Eur. J. Immunol. 24, 1692-1697, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession:
A; Status: pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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Residues: 1-199 <S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146 KKEPGHPWKWSNGKEFNNWFNVTGSDK----CVFLKNTEVSSMECEKNLYWICNK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 22.9 ses 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEDWYGYQRKCYFISTYKRSWTSAQNACSEHGATLAYIDSEKDMNFLKRYAGREEHWYGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCWIGL 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRHEGSFQVPVLCAVMNVVFITILIIALIALSVGQY----NCPGQYTFSMPSDSHVSSC
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   transmembrane
                             12p13
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22.9%;
   #status
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Pred. No. 5.2e-09;
3; Mismatches 76;
predicted
   √MMF
                                                                                                                    he group of macrophage/hepatic and processing.
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RESULT
T28141
C type lectin, B locus - chicken C;Specias: Gallus gallus (chicken) C;Date: 15-OCt-1999 #sequence_revi C;Accession: T28141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X53042; NID:g53104; PIDN:CAA37211.1; C;Superfamily: hepatic lectin; C-type lectin homology C;Reywords: glycoprotein; liver; transmembrane protein F;170-293/Domain: C-type lectin homology <LCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   asialoglycoprotein receptor - mouse
N;Alternate names: hepatic lectin
C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
C;Accession: S13165
R;Sanford, J.P.; Doyle, D.
Biochim. Biophys. Acta 1087, 259-261, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
S13165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-301 <SAN>
A; Cross-references: EMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: Mouse asialoglycoprotein receptor A; Reference number: S13165; MUID: 91027942 A; Accession: S13165
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                                                                                                                                                                                                                                                                                                                            152 LRTLTCQLAYFQSNGTEC-----CPVNWVEFGGSCYWFSRDGLTWAEADQYCQLENAHLL
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                    #sequence_revision 15-Oct-1999 #text_change
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21.6%; Pred. No. 1.8e-08;
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Pred. No. 3.6e-08;
29; Mismatches 72;
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Database :
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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     548
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V239_FOWPV
LECT_RAT
V008_FOWPV
KLR4_MOUSE
KUCR_RAT
PBCG_HUMAN
PAP3_MOUSE
KUCR_MOUSE
KUCR_MOUSE
KUCR_MOUSE
KUCR_MOUSE
KUCR_MOUSE
FGCV_CHICK
PAZR_BOVIN
PAP1_MOUSE
PAP1_MOUSE
                                                                                                                                                                                                                                                                                                             CLF2_HUMAN
LECI_MOUSE
MMGL_RAT
LECH_MOUSE
LY4A_MOUSE
NK12_MOUSE
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NKGE_HUMAN
NK13_RAT
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NKGC_HUMAN
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Compugen Ltd.
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(without alignments)
614.958 Million cell updates/sec
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P14370 fowlpox vir
Q60651 mus musculu
P27814 mus musculu
P27814 mus musculu
P27978 homo sapien
Q92778 homo sapien
Q92794 mus musculu
P70194 mus musculu
P70194 mus musculu
P70307 homo sapien
P49260 oryctolagus
Q60654 mus musculu
Q90953 gallus gall
P49259 bos taurus
P35230 mus musculu
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P26715
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R MIM; ...

IN TETERTO; IPROUISUT,

Pfam; PF00059; lectin\_c; 1.

R Pfam; PF00059; lectin\_c; 1.

DR SMART; SM00034; CLECT; 1.

EN PROSITE; PS00615; C\_TYPE\_LECTIN\_2; 1.

PROSITE; PS50041; C\_TYPE\_LECTIN\_2; 1.

EN PROSITE; PS50041; C\_TYPE\_LECTIN\_2; 1.

EN PROSITE; PS50041; C\_TYPE\_LECTIN\_2; 1.

EN PROSITE; PS50041; C\_TYPE\_LECTIN\_2; 1.

CYTOPLASMIC (POTENTIAL).

FT DOMAIN 1 31 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)

FT TRANSMEM 11 31 (POTENTIAL).

FT DOMAIN 98 176 (POTENTIAL).

EN PROSITE; PS50041; C\_TYPE LECTIN (LONG FORM).

EN PROSITE; PS50041; C\_TYPE LECTIN (LONG FORM).

EN PROSITE; PS50041; CLECTIN (LONG FORM).

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	UENC SUE C LINE LINE LINE Clar CCLA SUB MEM MEM SUB SIM DATI	LT 1 _HUMAN CD94 HUMAN O13241; O1-NOV-1997 O1-NOV-1997 15-DEC-1998 Natural kill receptor sub KLRD1 OR CD9 HOMO sapiens Eukaryota; M	136.5 136.5 136.5 134.5 134.5 133.5 133.5
Swiss Swiss Hoin Thisi Thisi Thisi This This This This T	pettneria; pri- petone; prod; sod; solil848; pubm s	ST (Rel. (Rel. (Rel. (Rel. 4. (Hum	13.3 13.3 13.3 13.3 13.3 13.1 13.1 13.1
try fin for t sta a 1 o 1 o 1 c CTTCTTCTTT G11 77	06; 06; 08, pubmed-75891 848; pubmed-75891 riguez A., Carret aracterization of related to the C- col. 25:2433-2437( pLAYS A ROLE AS LA-E MOLECULES BY CAN FORM DISULFID AR LOCATION: Type ECIFICITY: NATURA Y: CONTAINS 1 C-T NAME-PROW; NOTE- Y-//www.ncbi.nlm.n	NDARD; 35, Cre 35, Las 37, Las 37, Las 1s anti D, mem	165 321 331 163 175 175 175 2109 2109 2109 2109 2333
rote	758 arr. con he he he Arg. 243 arr. CULF. Ty. Arrunal nlm		
yright. It is possible of Bioinformat Institute. The Institute of Bioinformat Ittlong is not removed. Agreement (See isb-sib.ch).  c.  c.  c.  c.  c.  c.  c.  c.  c.	Med=7589107; ., Carretero M., Lopez zation of human CD94: to the C-type lectin s 433-2437(1955). ROLE AS A RECEPTOR FO ECULES BY NK CELLS AND DISULFIDE-BONDED HETE ION: Type II membrane Y: NATURAL KILLER CELL INS 1 C-TYPE LECTIN FA OW; NOTE=CD quide CD94 cbi.nlm.nih.gov/prow/c	ALIGNMENT PRT; 179 Led) red) rediannotation up n CD94 (KP43) r 1).	LITH_RAT FCE2_HUMAN FCE2_MOUSE ANP_HEMAM KLR3_MOUSE LITH_BOVIN FAP2_MOUSE LECH_CHICK FGCA_CHICK FGCA_CHICK FGCA_CHICK FGCA_CHICK FGCA_CHICK FGCA_CHICK FGCA_CHICK FGCA_CHICK FGCA_CHICK FGCA_CHUMAN
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Best Local
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CD69_MOUSE STANDARD
P37217;
01-0CT-1994 (Rel. 30, C
01-0CT-1994 (Rel. 30, I
16-0CT-2001 (Rel. 40, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
CARBOHYD
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                                   EMBL; L23638;
HSSP; P05451;
                                                                      the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                          recell activation critical related to
                                                                                                                                                                                                                                                                                                                                                                                                     Ziegler S.F., Ramsdell
Grabstein K.H., Hennen
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-93314711; PubMed-8100776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
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              InterPro;
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                                                                                                                                                                        ACQUIRED DURING LYMPHOID ACTIVATION.

INDUCTION: BY THE ACTIVATION OF TLYMPHOCYTES.

PTM: CONSTITUTIVE SER/THR PHOSPHORYLATION IN BOTH MATUR
THYMOCYTES AND ACTIVATED T LYMPHOCYTES (BY SIMILARITY).

SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
                                                                                                                                                                                                                                  SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
SUBCELLULAR LOCATION: Type II membrane protein.
TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T
B-CELLS, NATURAL KILLER CELLS, NEUTROPHILS AND PLATELETS.
DEVELOPMENTAL STAGE: EARLIEST INDUCIBLE CELL SURFACE GLYCOPH
                                                                                                                                                                                                                                                                                                          activation antigens.";
J. Immunol. 23:1643-1648(1993).
FUNCTION: INVOLVED IN LYMPHOCYTE PROLIFERATION AND FUNCTIONS AS
                                                                                                                                                                                                                                                                                                    CELLS, AND PLATELETS.
                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CSCLVAITLGLLTAVLLSVLLYQWILCQGSN--YSTCASCPSCPDRWMKYGNHCYYFSVE 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NFSRISSNSF----VQTCGAINKNG-LQASSCEVPLHGVCKK 186
                       MGI:88343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -- SQYLFPSFETFNTKNCIAYNPNGNALDESCEDKNRYICKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QKTWNESRHLCASQKSSLLQLQNTDELDFMS--SSQQFYWIGLSYSEEHTAWLWENGSAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLSLMA-TLGILLKNSFTKLSIEPAFTPGPNIELQKDSDCCSCQEKWVGYRCNCYFISSE
 PF00059;
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179 AA;
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                                                -; NOT_ANNOTATED_CDS
 lectin_c;
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                        cd69.
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132
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Rodentia;
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K.B., Farrah
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
; 1884D99E8D9583A7 CRC64;
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Pred. No. 9.9
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Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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T., Fanslow W.C., Sh
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                                                                                   (See http://www.isb-sib
                                                                                                          There are no rest
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a family of natural,
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URFACE GLYCOPROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murinae;
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l killer
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RESULT
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Best Local Similarity
Matches 52; Conserv
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P27811;
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DISULFID
DISULFID
CARBOHYD
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                    "Mouse NKR-P1. A family of genes selectively
lymphokine-activated killer cells.";
J. Immunol. 147:1701-1708(1991).
                                                                                                                                                                                                                                                                                             01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Natural killer cell surface protein P1-2 (NKR-P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
DOMAIN
-!- FUNCTION: MAY FUNCTION AS SIGNAL-TRANSMITTING
-!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
-!- SUBCELULAR LOCATION: Type II membrane protein
-!- TISSUE SPECIFICITY: NATURAL KILLER CELLS.
                                                            "CDNA CITE Identification 6.";
                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                              J. Immunol. 147:3229-3236(1991)
                                                                   "cDNA cloning of mouse NKR-P1 and genetic linkage Identification of a natural killer cell gene compl
                                                                                        Seaman W.E
                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                     LY55A OR LY55
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                                                          chromosome 6
                                                                                                     Yokoyama W.M., Ryan
                                                                                                                  MEDLINE=92013158; PubMed=1680927;
                                                                                                                                                                                                 MEDLINE-91349596; PubMed=1880421;
                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                     NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RGQKDHGTSIHFEKHHEG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                            CEVPLHGVCKK 186
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68
96
173
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                                                                                                      J.C.,
                                                                                                                                                                                                                                                   Chordata;
Rođentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.2%;
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           Type II membrane protein
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Pred. No. 1.
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C-TYPE LECTIN
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                                                                                                      J.J.,
                                                                                                                                                                                                                                                                                                                                                            227
                                                                                                       Smith H.R.C.,
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hes 79;
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PR (TYPE-II MEMBRANE)
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RESULT 4
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Pfam; PF00059; lectin.

SMART; SM0034; CLECT; 1.

SMART; SM00034; CLECTIN.2; FALSE_Nzu.

PROSITE; PS00615; C_TYPE_LECTIN.2; 1.

PROSITE; PS0064; C_TYPE_LECTIN.2; 1.

PROSITE; PS0064; C_TYPE_LECTIN.2; 1.

PROSITE; PS0064; C_TYPE_LECTIN.2; 1.

PROSITE; PS0064; C_TYPE_LECTIN.2; 1.

PROSITE; PS00615; C_TYPE_LECTIN.2; 1.

PROSITE; PS00615; C_TYPE_LECTIN.2; 1.

PROSITE; PS00615; C_TYPE_NZU...

PROSITE: PS00615; C_TYPE_NZ
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CARBOHYD
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P26715;
01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last seg
01-AUG-1992 (Rel. 41, Last ann
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CONFLICT
                                                                                                          SEQUENCE FROM N.A.
MEDLINE-91178434; Pubmed-2007850;
Houchins J.P., Yabe T., McSherry
                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                NKG2-A/NKG2-B type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the
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                                                                                                                                                                                                                                                                                                                                                                        NK receptor)
                                                                                        "DNA sequence
                                                                                                                                                                                                                                   NCBI_TaxID-9606;
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EMBL; M77753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154
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MGI:107540; Ly55a.
rPro; IPR001304; lectin_c.
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  173:1017-1020(1991)
                                                        II integral membrane
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27.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .48;
                                                                                     McSherry C., Bach
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C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
OF SIMILARITY.
OF SIMILARITY.
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
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S-> L (IN REF. 2).
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Pred. No. 4.2e-11;
                                                                                                                                                                                                                                                        Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                        proteins
                                                                               Bach F
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                                                                                  related cDNA clones
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                                                        human
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                                                        natural killer
                                                                                                                                                                                                                                                           Homo
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                                                                                                                                                               Matches
                                                                      Query Match
Best Local
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EMBL; X54868; CAA38650.1; -.
EMBL; U54786; AAB17133.1; JOINED.
EMBL; U54783; AAB17133.1; JOINED.
EMBL; U54784; AAB17133.1; JOINED.
EMBL; U54785; AAB17133.1; JOINED.
EMBL; AF023840; AAC17488.1; -.
                                                                                                                                                            CARBOHYD
CARBOHYD
VARSPLIC
SEQUENCE
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DISULFID
DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001304; lectin_c.
InterPro; IPR001304; lectin_c; 1.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS000615; C_TYPE_LECTIN_1; FALSE_NEG.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Receptor; Transmembrane; Multigene family; Signal-anchor; Receptor; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENOMICS 49:193-199(1998).

GENOMICS 49:193-199(1998).

FUNCTION: PLAYS A ROLE AS A RECEPTOR FOR THE RECOGNITION OF MHC CLASS I HLA-E MOLECULES BY NK CELLS AND SOME CYTOTOXIC T-CELLS.

CLASS I HLA-E MOLECULES BY NK CELLS AND SOME CYTOTOXIC T-CELLS.

SUBCULT: CAN FORM DISULFIDE-BONDED HETERODIMER WITH CD94.

SUBCELLULAR LOCATION: Type II membrane protein.

HATTERNATIVE PRODUCTS: THE NKG2-A AND -B PEPTIDES APPEAR TO BE ALTERNATIVE SPLICING PRODUCTS OF A SINGLE GENE.

HATTERNATIVE SPLICING PRODUCTS OF A SINGLE GENE.

HISSUE SPECIFICITY: NATURAL KILLER CELLS.

HISSUE SPECIFICITY: NATURAL KILLER CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plougastel B., Trowsdale J.;
"Sequence analysis of a 62-kb region overlapping the cluster of genes.";
                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
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SEQUENCE FROM N.A.
MEDLINE=96337918; PubMed=8753859;
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MEDLINE=98260668; PubMed=9598306;
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PT0373; PT0373.
VIYSMLELPTATQAQNDYGPQQKSSSSK--PSC-SCLVAITLGLLTAVLL---
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                                                   Similarity 55; Conser
                                                   Conservative
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                                              35;
                                                                                                                                                        C-TYPE LECTIN (LONG E
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...)
                                              Score 190; DE
Pred. No. 5.4e
35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR
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                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
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                                                                                         DB
                                                                      4e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     (TYPE-II MEMBRANE
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  -SYLLYQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NKGC_HUMAN STANDARD; PRT; 231 AA. P26717; O43802; P26717; O43802; O1-AUG-1992 (Rel. 23, Created) O1-MAR-2002 (Rel. 41, Last sequence update) O1-MAR-2002 (Rel. 41, Last annotation update) NKG2-C type II integral membrane protein (NKG
 Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LEC
PROSITE; PS50041; C_TYPE_LEC
                                                                                                                                                                  between the Swiss Institute of Bioinformatics and the Find the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                         -i- SUBUNIT: CAN FORM DISULFIDE-BONDED HETERODIMER WITH
-i- SUBCELLULAR LOCATION: Type II membrane protein.
-i- TISSUE SPECLETCITY: NATURAL KILLER CELLS.
-i- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glienke J., Sobanov Y., Brostjan C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encoding type II integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE-91178434; Pubmed-2007850;
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                        EMBL; AJ001684; CAA04922.:
EMBL; Y13055; CAA73498.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Houchins J.P., Yabe T., McSherry C., Bach F.H.; "DNA sequence analysis of NKG2, a family of rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN
                                                                                                                                       EMBL; X54869; CAA38651.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98350122; PubMed-9683661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                  FISSUE=Lymphoid;
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                                                                                                                                                                                                                                                                                                                                                   nitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.

FUNCTION: PLAYS A ROLE AS A RECEPTOR FOR THE RECOGNITION OF MHC
CLASS I HLA-E MOLECULES BY NK CELLS AND SOME CYTOTOXIC T-CELLS.
                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genomic organization of NKG2C, n natural killer gene complex.
                                                                             602891;
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                                                                                        PT0374; PT0374.
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PS00615; C_TYPE_LECTIN_1; PS50041; C_TYPE_LECTIN_2;
                                                          IPR001304; lectin_c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173:1017-1020(1991).
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48:163-173(1998).
                                                                                                                      CAA04922.1; -.
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Primates;
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               FALSE_NEG
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CONFLICT
SEQUENCE
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P26718;
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DISULFID
                                                                           SEQUENCE FROM N.A.

MEDLLINE-91178434; PubMed-2007850;

MEDLLINE-91178434; PubMed-2007850;

Houchins J.P., Yabe T., McSherry C., Bach F.H.;

"DNA sequence analysis of NKG2, a family of related cDNA clones encoding type II integral membrane proteins on human natural ki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein DOMAIN
This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                           MEDLINE=98350122; PubMed=9683661; Glienke J., Sobanov Y., Brostjan C., Lehrach H., Hofer E., Francis F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                          - i - SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
                                                                                                                                                                                                                        *The genomic organization of NKG2C,
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE-98350122;
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231 AA;
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(Rel. 23, Last sequence update)
(Rel. 41, Last annotation updat
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Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; I
PROSITE; PS50041; C_TYPE_LECTIN_2;
PROSITE; PS50041; C_TYPE_LECTIN_2;
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                 SEQUENCE FROM N.A.
MEDLINE-94103823; PubMed-8276468;
Adamklewicz T.V., McSherry C., Bach F.
"Natural killer lectin-like receptors
distinct from C-type lectins.";
                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Immunogenetics [2]
                                                                                    NCBI_TaxID=9606
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                                                                                                                                                                                                                                                                   GSILSPNLLTITEMQKGDCALYASSFKGYTENCSTPN 207
                                                                                                                                                                                                                                                                                                               FFDESKNWYESQASCMSQNASLLKVYSKEDQDLLK--LVKSYHWMGLVHIPTNGSWQWED
                                                                                                                                                                                                                                                                                                                                   FSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCWIGL---RNNSGWRWED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            602893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S19110; S19110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AJ001687; CAA04925.1; -.
AJ001688; CAA04925.1; JOINED
AJ001689; CAA04925.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                               216
                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73
98
99
127
189
131
163
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52
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                                                                                                                                                              35, Created)
35, Last sequence update)
41, Last annotation update)
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213
110
211
211
203
131
163
                                                                                                                                                                                                                                                                                                                                                                                                                  17.6%;
26.8%;
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                                                                                                                                                      membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                               W.
                                                                                                                                                                                                                                                                                                                                                                                                       31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLUÍAR (POTENTIAL).
C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTE
N-LINKED (GLCNAC. . .) (POTE
N-LINKED (GLCNAC. . .) (POTE
                                                                                                                                                                                                                                                                                        SSNSFVQTCGAIN 167
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 180; DB 1;
Pred. No. 4.4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                             PRT;
                                          Bach F.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             C22F6BD533D7800E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         family; Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FALSE_NEG.
                                                                                                                                                                                                             240
                                have
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                                                                                                                                                    (NKG2-D
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                               Houchins J.P.;
e divergent carboxy-termini,
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                                                                                                                                                                                                                                                                                                                                                                                                                          Length 216
                                                                                                                                                    activating
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                                                                                                          Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                      32;
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Best Local :
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                                              NK13_RAT
P27471;
P27471;
01-AUG-1992
01-AUG-1992
01-JUN-1994
                                                                                                                RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
DISULFID
      3.2.3).
Rattus norvegicus (Rat)
 Eukaryota; Metazoa;
                                      Natural killer
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00059; lectin_c; 1.

SMART; SM00034; CLECT; 1.

PROSITE; PS000615; C_TYPE_LECTIN_1; FALSE_NEG
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outsithe European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIM; 602892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- SUBUNIT: CAN FORM DISULFIDE-BONDED HETERODIMER WITH CD94
-i- SUBCELLULAR LOCATION: Type II membrane protein.
-i- TISSUE SPECIFICITY: NATURAL KILLER CELLS.
-i- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The genomic organization of NKG2C, human natural killer gene complex."; Immunogenetics 48:163-173(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM; 004034,
InterPro; IPR001304; lectin_c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glienke J., Sobanov Y., Brostjan C.,
Lehrach H., Hofer E., Francis F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-98350122; PubMed-9683661;
                                                                                                                                                                                                                122
                                                                                                                                                                                     138 NSGWRWEDGSPLNFSR--ISSNSFVQTCGAINKNGLQASSC
                                                                                                                                                               180
                                                                                                                                                                                                                                        80
                                                                                                                                                                                                                                                                  67
                                                                                                                                                                                                                                                                                      24 PQQKSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWILCQGSNYST----CASCPSCPDRW 79
                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                           ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: PLAYS A ROLE AS A RECEPTOR FOR THE RECOGNITION OF CLASS I HLA-E MOLECULES BY NK CELLS AND SOME CYTOTOXIC T-CEI
                                                                                                                                                                                                              SSHHPWVTINGLAFKHEIKDSDHAERNCAMLHVRGLISDQC
                                                                                                                                                                                                                                      MKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDN-QEMSLLQVFLSEAFCWIGL-RN 137
                                                                                                                                                                                                                                                                PPEKLTAEVLGIICIV-----LMATVLKTIVLIPFLEQNNSSPNTRTQKARPCGHCPEEW 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AJ001685; CAA04923.1;
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                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane;
                                 (Rel. 23, Created)
(Rel. 23, Last sequence update)
(Rel. 29, Last annotation update)
ler cell surface protein P1-3.2.3
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116
117
207
207
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149
                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                  STANDARD;
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230
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220
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149
 Chordata;
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93
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28.6%;
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                                                                                                                                                                                                                                                                                                                                                                               MW;
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C-TYPE LECTIN (
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                Score 178.5; DB 1;
Pred. No. 6.9e-10;
0; Mismatches 70;
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N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POSIGNAL-ANCHOR (POTENTIAL).
Craniata; Vertebrata;
                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                               20691FB21274D8A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                family; Signal-anchor; Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Steffens C., Nguyen
                                                                                                  223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce,
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                                     (NKR-P1
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) (POTENTIAL).
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                                    3.2.3) (Antigen
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                                                                                                                                                                                                                                                                                                                                         240;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for
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RESULT 9
MMGL_MOUSE
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AC P49300
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Best Local
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MMGL_MOUSE P49300;
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DISULFID
DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
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PROSITE; PS50041; C_TYPE_LECTIN_2; I
Glycoprotein; Antigen; Transmembrane; Signal-anchor; Lectin.
DOMAIN
1 43 CYTOPLASMIC (POTENTIAL).
TRANSMEM 44 63 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by anc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M62891; AAA41710.1; -. PIR; A35917; A35917. InterPro; IPR001304; lectin_c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Giorda R., Rudert W.A., Vavassori C., Chambers Hiserodt J.C., Trucco M.;
"NKR-PJ, a signal transduction molecule on natu Science 249:1298-1300(1990).

1- FUNCTION: MEDIATES TRANSMEMBRANE SIGNALING (NK) CELLS- AND SO MAY ACT AS A RECEPTOR ABLTRIGGER NK CELL ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=90378305; PubMed=2399464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                    212 K
                                                                                                                                              153
                                                                                                                                                                          131
                                                                                                                  186
                                                                                                                                                                                                      93
                                                                                                                                                                                                                                                            35
                                                                                                                                                                                                                                                                                      24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE SPECIFICITY: NATÜRAL KILLER CELLS.
MISCELLANEOUS: LIGAND BINDING MAY BE CALCIUM DEPENDENT.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Type II membrane
                                                                                                                ~
                                                                                                                                            -WIGLSYTLSDENWKWINGSTLNSDVLSITGDTEKDSCASVSQDKVLSESCDSDNIWVCQ
                                                                                                                                                                      CWIGLR---NNSGWRWEDGSPLNFS--RISSNSFVQTCGAINKNGLQASSCEVPLHGVCK 185
                                                                                                                                                                                                                                                                                     POOKSSSSKPSCSCLVAITLGLL-TAVLLSVLLYQ----WILCOGSNYSTCASCPS--
                                                                                                                                                                                                  KCPKDWLSHRDKCFHVSQTSITWKESLADCGGKGATLLLVQDQEELRFLRNLTKRISSSF
                                                                                                                                                                                                                                                         PRSHRLALKLSCAGLILLVLALVGMSILVRVLVQKPSVEPCRVLIQ-ENLSKTGS-PAKL 92
                                                                                                                                                                                                                             -CPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVF---LSEAF 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF00059; lecti
                                                                                                                  186
                                                                                                                                                                                                                                                                                                                   l Similarity
49; Conserv
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                                                                                      212
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143
169
                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                          AA;
                STANDARD;
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212
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169
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27.1%;
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                                                                                                                                                                                                                                                                                                                                                                                          MW;
                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

C-TYPE LECTIN (LONG FORM).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLUNAC. . ) (POTENTIAL).

N-LINKED (GLUNAC. . ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                   44;
                                                                                                                                                                                                                                                                                                              Score 175.5; DB 1;
Pred. No. 1.2e-09;
                PRT;
                304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               restrictions
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MBL outstation -
                                                                                                                                                                                                                                                                                                                 21;
                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                            211
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Query Match
Best Local S
Matches 39
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CARBOHYD
SEQUENCE
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DOMAIN
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Oda S., Sato M., Toyoshima S., Osawa T.;
Oda S., Sato M., Toyoshima S., Osawa T.;
Purification and characterization of a lectin-like molecule specific "purification and characterization of a lectin-like molecule specific for galactose/N-acetyl-galactosamine from tumoricidal macrophages.";
J. Biochem. 104:600-605(1988).
-!- FUNCTION: RECOGNIZES TERMINAL GALACTOSE AND N-ACETYLGALACTOSAMINE UNITS. MAY PARTICIPATE IN THE INTERACTION BETWEEN TUMORICIDAL MACROPHAGES AND TUMOR CELLS.
-!- SUBBUNTP: HOMO-OLICOMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Macrophage asialoglycoprotein-binding protein (M-ASGP-BP) (Macrophage galactose/N-acetylgalactosamine-specific lectin) (MMGL).
MGL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001304; lectin_c. Pfam; PF00059; lectin_c; 1. SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; S36676; AAB22171.1;
HSSP; P06734; 1KJE.
MGD; MGI:96975; Mg1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-slb.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sato M., Kawakamyi K., Osawa T., Toyoshima S.; "Molecular cloning and expression of cDNA encoding a galactose/N-acetylgalactosamine-specific lectin on mouse tumoricidal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C3H/HEN;
MEDLINE=92268032; PubMed=1587794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00615; C_TYPE_LECTIN_1; 1. PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 102-120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               macrophages.";
156 LTCQLANLKNNGSEVACCPLHWTEHEGSCYWFSESEKSWPEADKYCRLENSHLVVVNSLE
                                                                                                                                                                                                                                                                                                                                                                                                                              ectin;
                                            59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Type II membrane protein. TISSUE SPECIFICITY: IS EXPRESSED ON THE SURFACE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MACROPHAGES.
                                          ILCQGSNYSTCAS-CPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQ 117
                                                                                    Similarity 27.5
39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111:331-336(1992).
                                                                                                                                                                                                                                      57
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274
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184
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56
                                                                                                                                                                                              34596
                                                                                                          17.1%;
27.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane;
                                                                                                                                                                                              MW;
                                                                                    27;
                                                                                  Score 174.5;
Pred. No. 2.1e
27; Mismatches
                                                                                                                                                                                            BY SIMILARITY.

N-LINKED (GLCNAC. . .) (P
N-LINKED (GLCNAC. . .) (P
S79CD12C34F5BCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR
C-TYPE LECTIN
                                                                                                                                                                                                                                                                            BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                Calcium; Signal-anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          There are no restrictions on ng as its content is in no
                                                                                                            le-09;
                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
                                                                                                                              DB 1;
                                                                                      61;
                                                                                                                            Length
                                                                                      Indels
                                                                                                                                                                                                                (POTENTIAL)
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                                                                                                                              304;
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                                                                                    15;
                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN)
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RESULT NKGE_HH ID AC OC OC EH COC EH 
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; E
NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                            NKGE_HUMAN
Q07444;
Q1-NOV-1997
Q1-NOV-1997
Q1-MAR-2002
NKG2-E type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
                 MEDLINE-94102823; PubMed-8276468; Adamkiewicz T.V., McSherry C., Bach F. "Natural killer lectin-11ke receptors distinct from C-type lectins."; Immunogenetics 39:218-218(1994).
                                                                                                                                                                                                                                                         receptor).
KLRC3 OR NKG2E.
                                                                                                                                                                                                                                                                                                                                                                                                                                HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the Buropean Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam: PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE: PS00615; C_TYPE_LECTIN_1;
PROSITE: PS50041; C_TYPE_LECTIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X54870; CAA38652.1; --
EMBL; AJ0001687; CAA04925.1; --
EMBL; AJ001688; CAA04925.1; JOINED
EMBL; AJ001689; CAA04925.1; JOINED
                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSPLNFSRI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCWIGL---RNNSGWRWED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CFIAVAMGIRFIIMVAIWSAVFLNSLFNQEVQIP----LTESYCGPCPKNWICYKNNCYQ 112
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S19110; S19110.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FFDESKNWYESQASCMSQNASLLKVYSKEDQDLLK--LVKSYHWMGLVHIPTNGSWQWED
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                                                                                                                                                                                                                                                                                                                  (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                  II integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                         Chordata;
Primates;
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26.8%;
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BY SIMILARITY.
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -SSNSFVQTCGAIN
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 180; DB 1;
Pred. No. 4.4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL)
C-TYPE LECTIN (LONG FORM)
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II M
                                                                                                                                                                                         Catarrhini;
                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C22F6BD533D7800E CRC64;
                                                                                                                                                                                                                                                                                              ation update)
protein (NKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    family; Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                        240
                                                                                 Ή.,
                                                               have
                                                                                                                                                                                                                                                                                                (NKG2-D
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                                                             Houchins J.
e divergent
                                                                                                                                                                                         Hominidae;
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(POTENTIAL).
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P
                                                               carboxy-termini,
                                                                                                                                                                                         Homo.
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                                                                                                                                                                                                        RESULT
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Best Local S
Matches 46
                                                                           "NK13_RAT
P27471;
01-AUG-1992
01-AUG-1992
01-JUN-1994
                                                                                                                                                                                   RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
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DISULFID
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. The use by non-profit institutions as not removed modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The genomic organization of NKG2C, E, F, and human natural killer gene complex."; Immunogenetics 48:163-173(1998).
-i- FUNCTION: PLAYS A ROLE AS A RECEPTOR FOR CLASS I HLA-E MOLECULES BY NK CELLS AND STREET THE CLASS IN THE PROPERTY OF T
Rattus norvegicus (Rat)
Eukaryota; Metazoa; Cho
                                                            Natural killer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glienke J., Sobanov Y., Brostjan C.,
Lehrach H., Hofer E., Francis F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG PROSITE; PS50041; C_TYPE_LECTIN_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM; 602892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Type II membrane protein.
-!- TISSUE SPECIFICITY: NATURAL KILLER CELLS.
-!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.: MEDLINE=98350122; PubMed=9683661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
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                                                                                                                                                                                                                                                                                                      NSGWRWEDGSPLNFSR--ISSNSFVQTCGAINKNGLQASSC
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                                                                                                                                                                                                                                                                                                                                                              MKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDN-QEMSLLQVFLSEAFCWIGL-RN 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PQQKSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWILCQGSNYST----CASCPSCPDRW
                                                                                                                                                                                                                                                                SSHHPWVTINGLAFKHEIKDSDHAERNCAMLHVRGLISDQC
                                                                                                                                                                                                                                                                                                                                                                                                                             PPEKLTAEVLGIICIV-----LMATVLKTIVLIPFLEQNNSSPNTRTQKARPCGHCPEEW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AJ001685; CAA04923.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR001304; lectin_c
                                                                             (Rel.
(Rel.
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                                                              cell surface
                                                                                                                                                                STANDARD;
                                                    23, Created)
23, Last sequence update)
29, Last annotation update)
29, or face protein P1-3.2.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240
230
128
128
220
100
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179
  Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70
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28.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 178.5; DB 1
Pred. No. 6.9e-10;
0; Mismatches 7(
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N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
; 20691FB21274D8A6 CRC
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SIGNAL-ANCHOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     family; Signal-anchor;
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ng as its content is in no
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    Euteleostomi;
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RESULT 9
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A Giorda R., Rudert W.A., Vavassori C., Chambers W.H.,
A Hiserodt J.C., Trucco M.;
A Hiserodt J.C., Trucco M.;
T "NKR-P1, a signal transduction molecule on natural killer cells.";
C -: FUNCTION: MEDIATES TRANSMEMBRANE SIGNALING IN NATURAL KILLER
C (NK) CELLS. AND SO MAY ACT AS A RECEPTOR ABLE TO SELECTIVELY
C TRIGGER NK CELL ACTIVITY.
C -: SUBCULTE, HOMODIMER.
C -: SUBCULTURA LOCATION: Type II membrane protein.
C -: TISSUE SPECIFICITY: NATURAL KILLER CELLS.
C -: MISCELLANEGUS: LIGAND BINDING MAY BE CALCIUM DEPENDENT.
C -: SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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CARBOHYD
  MMGL_MOUSE
P49300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PQQKSSSSKPSCSCLVAITLGLL-TAVLLSVLLYQ-----WILCQGSNYSTCASCPS--
                                                                                                                                                                                                                                                 -WIGLSYTLSDENWKWINGSTLNSDVLSITGDTEKDSCASVSQDKVLSESCDSDNIWVCQ
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                                                                                                                                                                                                                                                                                                                                                                                             -CPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVF---LSEAF 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRSHRLALKLSCAGLILLVLALVGMSILVRVLVQKPSVEPCRVLIQ-ENLSKTGS-PAKL
                                                                                                                                                   212
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PSO041; C_TYPE_LECTIN_2; 1.
PS50041; C_TYPE_LECTIN_2; 1.
tein; Antigen; Transmembrane; Signal-anchor; Lectin.
tein; A CYTOPLASMIC (POTENTIAL).
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                            STANDARD;
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C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
OF SIMILARITY.
N-LINKED (GLCNAC. . .) (POTE N-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 175.5; DB 1
Pred. No. 1.2e-09;
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                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 223;
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Query Match
Best Local
Matches 3
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CARBOHYD
SEQUENCE
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01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Macrophage asialoglycoprotein-binding protein (M-ASGP-B
galactose/N-acetylgalactosamine-specific lectin) (MMGL)
MGL.
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Pfam; PF00059; lectin_c;
SMART; SM00034; CLECT; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C3H/HEN;
MEDLINE=89197865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sato M., Kawakamyi K., Osawa T., Toyoshima "Molecular cloning and expression of cDNA acetylgalactosamine-specific lectin on mous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:96975; Mgl.
InterPro; IPR001304; lectin_c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; S36676; AAB22171.1; HSSP; P06734; 1KJE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-92268032; PubMed-1587794; Sato M., Kawakamyi K., Osawa T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                             ectin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       European Bioinformatics Institute. The by non-profit institutions as long ified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MACROPHAGES AND TUMOR CELLS.
SUBUNIT: HOMO-OLLIGOMER:
SUBCELLULAR LOCATION: Type II membrane proteig.
TISSUE SPECIFICITY: IS EXPRESSED ON THE SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: RECOGNIZES TERMINAL GALACTOSE AND N-ACETYLGALACTOSAMINE UNITS. MAY PARTICIPATE IN THE INTERACTION BETWEEN TUMORICIDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MACROPHAGES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
ILCQGSNYSTCAS-CPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQ 117
                                          Similarity 27.9
                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sato M.,
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                                                                                                                                                    ΑA;
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                                                                                                                                                    34596 MW;
                                                               17.1%;
27.5%;
                                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137-151.
                                          27;
                                                                                                                                                EXTRACELLULAR (POTENTIAL).
C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
OF COLUMN (PO'N-LINKED (GLCNAC. . . ) (PO'N-LINKED (GLCN
                                          Score 174.5; DB 1
Pred. No. 2.1e-09;
Pred. No. 2.6 61
                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL SIGNAL-ANCHOR (TYPE-II
                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA encoding a galactose/N-
on mouse tumoricidal
                                                                                                                                                                                                                                                                                                                                                                                               Calcium; Signal-anchor.
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                                                                                                                                                          Santis A., Lopes-Cabrera M., Hamann J., Strauss M., Sanchez-Madr. Santis A., Lopes-Cabrera M., Hamann J., Strauss M., Sanchez-Madr. Structure of the gene coding for the human early lymphocyte activation antigen CD69: a C-type lectin receptor evolutionarily related with the gene families of natural killer cell-specific
                                                                                                                                                                                                                                                                                                                                                         MEDLINE-93314711; PubMed-8100776;
Ziegler S.F., Ramsdell F., Hjerrild K.A.,
Grabstein K.H., Hennen K.B., Farrah T., F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
16-OCT-2091 (Rel. 40, Last annotation update)
Early activation antigen CD69 (Early T-cell activation antigen (GP32/28) (Leu-23) (MLR-3) (EAl) (BL-AC/P26) (Activation induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD69_HUMAN
Q07108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of the C-type animal lectin superfamily of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hamann J., Fiebig H., Strauss M.; "Expression cloning of the early activation antigen CD69, a type integral membrane protein with a C-type lectin domain."; J. Immunol. 150:4920-4927(1993).
                                                                                                                                                 receptors.";
                                                                                                                                                                                                                           MEDLINE-94298875; PubMed-8026529;
                                                                                                                                                                                                                                           TISSUE=Placenta;
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                Alderson M.R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-93267093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=BIOOD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    molecule) (AIM)
                                                                                                                                                                                                                                                                                                         "Molecular characterization of the early 
type II membrane glycoprotein related to 
cell activation antigens.";
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-93340630; PubMed-8340758;
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                        SUBCELLULAR LOCATION: Type II membrane protein.
TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED B-CELLS, NATURAL KILLER CELLS, NEUTROPHILS, EOSINOPHILS, I
                                                                                     J. Immunol. 24:1692-1697(1994).
FUNCTION: INVOLVED IN LYMPHOCYTE
ELIGNAL TRANSMITTING RECEPTOR IN L
CELLS, AND PLATELETS.
B-CELLS, NATURAL KILLER CELLS,
LANGERHANS CELLS AND PLATELETS
DEVELOPMENTAL STAGE: EARLIEST 1
                                                                           SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cular cloning, expression, and chromosomal localization of the earliest lymphocyte activation antigen AIM/CD69, a new member
                                                                                                                                                                                                                                                                                                                                                                                                                                         Med.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             brera M., Santis A.G., Fernandez-Ruiz Sanchez-Mateos P., Sanchez-Madrid F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                        178:537-547(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                      23:1643-1648(1993).
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
INDUCIBLE CELL SURFACE GLYCOPROTEIN
                                                                                                       LYMPHOCYTES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96-103; 128-146 AND 189-199
                                                                                                                     PROLIFERATION
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                                                                                                                                                                                                                                                                                                                                                             Fanslow
                                                                                                                                                                                                                                                                                                                 activation antigen CD69: a a family of natural killer
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'C., Shevach!
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                                                                                                                     FUNCTIONS AS
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                             D T CELLS,
EPIDERMAL
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Best Local
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EMBL; Z22576; CAA83017.1;
EMBL; Z30426; CAA83017.1;
EMBL; Z30440; CAA83017.1;
EMBL; Z30427; CAA83017.1; J
EMBL; Z30429; CAA83017.1; J
EMBL; Z30429; CAA83017.1; J
EMBL; Z30429; CAA83017.1; J
                                                                                   029478;
01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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                                           C-type lectin s
CLECSF2 OR AICI
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SEQUENCE
    Eukaryota; Metazoa;
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                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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PROSITE: PS50041; C_TYPE_LECTIN_2; 1
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INDUCTION: BY ANTIGENS, MITOGENS OR ACTIVATORS
SURFACE OF AND B LYMPHOCYTES. BY INTERACTION
P75 IL-2R ON THE SURFACE OF NK CELLS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DATABASE: NAME-PROW; NOTE-CD guide CD69 entry; WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd69.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTM: CONSTITUTIVE SER/THR PHOSPHORYLATION THYMOCYTES AND ACTIVATED T LYMPHOCYTES.
                                                                                                                                                                                                                                                                               KKEPGHPWKWSNGKEFNNWFNVTGSDK----CVFLKNTEVSSMECEKNLYWICNK
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173
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                            (Human)
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199
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194
186
    Chordata;
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MW; 172E2699D2FB8DFB CRC64;
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EXTRACELLULAR (
C-TYPE LECTIN (
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    Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X96719
MIM; 603242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -:- SUBCELLULAR LOCATION: Type II membrane protein (Pro-
-:- TISSUE SPECIFICITY: Expressed preferentially in lyn
and in most hematopoletic cell types.
-:- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
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SEQUENCE FROM N.A.
MEDLINE-97190245; PubMed-9038101;
The second of t
                                                                                                                                                                                      01-MAR-1992 (Rel.
01-MAR-1992 (Rel.
30-MAY-2000 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00059; lectin_c; SMART; SM00034; CLECT; 1
                                                                                                                                                                                                                                                    P24721;
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                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                Asialoglycoprotein
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SEQUENCE * FROM N.A
                                        NCBI_TaxID=10090;
                                                                                                      Mus musculus (Mouse).
                                                                                                                            ASGR2 OR ASGR-2
                                                                                                                                                                                                                                                                     ECI_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                  L---RNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPLHGVCKK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CPYDWIGFQNKCYYFSKEEGDWNSSKYNCSTQHADLTIIDNIEEMNFLRRYKCSSDHWIG
                                                                                                                                                                                                                                                                                                                                                                            LKMAKNRTG-QWVHGA--TFTKSFGMRGSEGCAYLSDDGAATARCYTERKWICRK
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39,
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                                                              Chordata;
Rodentia;
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Last annotation updat
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EXTRACELLULAR (POTENTIAL).

C-TYPE LECTIN

BY SIMILARITY.

BY SIMILARITY.

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BY SIMILARITY.

N-LINKED (GLCNAC. . . ) (POTENTIAL).

N-LINKED (GLCNAC. . . ) (POTENTIAL).
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Pred. No. 4e-0
24; Mismatches
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CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE
                                                           Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                    (Hepatic
                                                                                                                                                                                                                                                                       PRT;
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n lymphoid
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                                                                Euteleostomi;
; Murinae; Mus
                                                                                                                                                                  (ASGP-R)
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InterPro; IPR001304; lectin_c.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
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PIR; S13165; S13165
HSSP; P06734; 1KJE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                       GGGEDCAEILSDGHWNDNFCQQVNRWVCEKRR
                                                                                                                                                                                                                                                                                                                KSSSKPSCSCLVAI ---- TLGLLTAVLL---
                                                              ----TCGAINKNG-LQASSCEVPLHGVCKKVR 188
                                                                                                           VINSREEQDFVVKHRSQFHIWIGLTDRDGSWKWVDGTDYR-
                                                                                                                                                                                                                                                                                                                                                                              Similarity
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CYTOPLASMIC
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Pred. No. 1.
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"Mouse asialoglycoprotein receptor cDNA sequence: conservation of receptor genes during mammalian evolution." Blochim. Blophys. Acta 1087:259-261(1990).

-i- FUNCTION: MEDIATES THE ENDOCYTOSIS OF PLASMA GLYCOPROTEINS TO WHICH THE TERMINAL SIALIC ACID RESIDUE ON THEIR COMPLEX CARBOHYDRATE MOIETIES HAS BEEN REMOVED. THE RECEPTOR RECOGNIZES TERMINAL GALACTOSE AND N-ACETYLGALACTOSAMINE UNITS. AFTER LIGAND BINDING TO THE RECEPTOR, THE RESULTING COMPLEX IS INTERNALIZED AN TRANSPORTED TO A SORTING ORGANELLE, WHERE RECEPTOR AND LIGAND ARE DISASSOCIATED. THE RECEPTOR THEN RETURNS TO THE CELL MEMBRANE
                                                                                          SUBCELLULAR LOCATION: Type II membrane protein. TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN HEPATIC
BINDING
                                                                                              PARENCHYMAL
                                                                                                                                                                                                                                                                                   D AND
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(See http://www.isb-slb.ch/announce/ are no restrictions EMBL żs Ω collaboration 'n commercial ņ 9 way

Lectin; Glycoprotein; Receptor; Endocytosis; Transmembrane;

BY SIMILARITY.
BY SIMILARITY.
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N-LINKED (GLCNAC. . . ) (POT
N-LINKED (GLCNAC. . . ) (POT
N-LINKED (GLCNAC. . . ) (POT (POTENTIAL). (LONG FORM). (POTENTIAL). (POTENTIAL). MEMBRANE PROTEIN)

KETFSNFSSSTLMEFGALDTLGGSTNAILTSWLAQLEEKQQQLKADHSTLLFHLKHFPMD VITDNQEMSLLQVFLSEAFCWIGLRNNSG-WRWEDGSPLNFSRISSNSFVQ---LRTLTCQLAYFQSNGTEC-----CPVNWVEFGGSCYWFSRDGLTWAEADQYCQLENAHLL -QWILCQ----GSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLL 111 Db 1.1e-08; 72; SNYRNWAFTQPDNWQGHEQ Length 301; Indels SVLLY-----56; Gaps 265 161 151 56

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Best Local s
Matches 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ii M., Kawasaki T., Yamashina I.;

"Structural similarity between the macrophage lectin galactose/N-acetylgalactosamine and the hepatic asial binding protein.";
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01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Macrophage asialoglycoprotein binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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Rattus norvegicus (Rat)
Eukarvota. wata---
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MEDLINE-90293078; PubMed-2358462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RΑΤ
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
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103 CLARDSHLLVITDNQEMSLLQVFLSEAFCWIGLRNNSG-WRWEDGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Type II membrane protein. SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: RECOGNIZES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: HOMO-OLIGOMER
                                                   LKTLTCQLASL----
                                                                                              LGLLTAVLLSVLLYQWILCQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEF 102
                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                            59
174
175
203
276
                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                     306
300
186
298
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58
                                                                                                                                                                                                                                                                            34242 MW;
                                             -----KNNGSAVAC--CPLHWMEHEGSCYWFSQSGKPWPEADKY 202
                                                                                                                                                                           16.1%;
32.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMMUN. 155:720-725(1988).
ES TERMINAL GALACTOSE AND N-ACETYLGALACTOSAMINE
                                                                                                                                                                                                                                                                      (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

C-TYPE LECTIN (LONG FORM).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

OF THE CONTROL OF THE 
                                                                                                                                                    18;
                                                                                                                                              Score 164.5; DB:
Pred. No. 1.9e-08.
8; Mismatches 4:
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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                                                                                                                                                                                               DB 1;
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RESULT 14
LECH_MOUSE
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                                                                                               EMBL; D13517; BAA02734.1; -.
EMBL; U09362; AAB60440.1; -.
EMBL; U08372; AAB60440.1; -.
PIR; S29855; S29855
HSSP; P20693; 1HLJ.
MGD; MGI:88081; ASGI1.
MGD; MGI:88081; ASGI1.
InterPro; IPR001304; lectin_c.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Lectin; Glycoprotein; Receptor; Endocytosis; Transmembrane;
                                                                                                                                                                                                                                                                               This
 DOMAIN
                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                       modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASGRI OR ASGRI (Mouse).
Mus musculus (Mouse).
Theria; Metazoa; Chordata; Metazoa; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LECH_MOUSE STANDARD; PRT; 283 AA P34927; Q64363; 01-FEB-1994 (Rel. 28, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation updat
                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence."
                                  DOMAIN
                                                                                                                                                                                                                                                                      between
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                                           [NIT_MET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95047431; PubMed=7958950;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Takezawa R., Shinzawa K., watanabe Y., Akaike T.,
Totermination of mouse major asialoglycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=93176818; PubMed=8439566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Asialoglycoprotein
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                                                                                                                                                                                                                                                                                                     MISCELLANEOUS: CALCIUM IS REQUIRED FOR LIGAND BINDII SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
                                                                                                                                                                                                                                                         European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Type II membrane protein.
TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN HEPATIC PARENCHYMAL
                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CQLENSNLVVVNSLAEQNFLQTHMGSVVTWIGLTDQNGPWRWVDGT
                                                                                                                                                                                                                                    non-profit institutions as long and this statement is not removed.
                                                        Signal-anchor;
                                                                                                                                                                                                                                                                   the Swiss Institute of Bioinformatics
 60
                    39
39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Liver;
 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor 1 (Hepatic
                     38
59
                                                        Phosphorylation.
                    CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                           BY SIMILARITY
 EXTRACELLULAR
            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata;
Sciurognathi; Muridae;
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Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248
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                                                                                                                                                                                                                                                                      EMBL
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RESULT 15
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Best Local Similarity
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DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
CONFLICT
                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE-89140367; PubMed=2783949;
Chan P.-Y., Take1 F.;
"Molecular cloning and characterization of a novel surface antigen, YE1/48.";
J. Immunol. 142:1727-1736(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
SITE
                                                                                                                                                                                                                                                                      MEDLINE-89309828; PubMed-2787364;
Yokoyama W.M., Jacobs L., Kanagawa O., Shevach E.M., Cohen D.I.;
"A murine T lymphocyte antigen belongs to a supergene family of
II integral membrane proteins.";
J. Immunol. 143:1379-1386(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
T-cell surface glycoprotein YEI/48 (T lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LY4A_MOUSE P20937;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 CPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCWIG 134
                                                                                                                                                                                                      SUBUNIT: HOMODIMER; DISULFIDE-LINKED. SUBCELLULAR LOCATION: Type II membran
                                                                                                                                                                                                                                FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS ALLELES. INHIBITS THE ACTIVITY OF NK CELLS THUS CELL LYSIS.
                                                                                                                                                                SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
                                                                                                                                                                           TISSUE SPECIFICITY: HIGH, NORMAL LYMPHOCYTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CPINWVEYEGSCYWFSSSYRPWTEADKYCQLENAHLVVVTSRDEQNFLQRHMGPLNTWIG
A30573, A30573.
              M25775; AAA40578.1;
M25812; AAA37242.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OR LY49A OR LY-49A OR LY49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   283
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150
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35.1%;
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IGH, IN T LYMPHOMA
                          ALT_SEQ
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ENDOCYTOSIS SIGNAL (POTENTIAL).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

I -> T (IN REF. 1).
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Pred. No. 2.1e-08;
7; Mismatches 30;
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                                                                                                                                                                                        membrane protein.
T LYMPHOMA LINES,
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Search completed:
Job time: 232 sec

September

9,

2002,

15:03:58

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/R MGD; MGI:101907; Klral.

/R InterPro; IPR001304; lectin_c.

DR Pfam; PF00059; lectin_c; 1.

DR SMART; SM00034; CLECT; 1.

DR PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.

DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.

T-cell; Glycoprotein; Antigen; Transmembrane; Cell adhesion;

T-cell; Glycoprotein; Receptor; Multigene family.

CYTOPLASMIC (PROBABLE).

CYTOPLASMIC (PROBABLE).
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                                                                                                                                                                                            VIYSMLELPTATQAQNDYGPQQKSSSSKPS---CSC---LVAITLG-----LLTAV-LLS 52
GNCDQVFICICGK
                      SSCEVPLHGVCKK 186
                                                                LQVFLSEAFCWIGL---RNNSGWRWEDGSPLNFSRISSNSFVQT----CGAINKNGLQA 173
                                                                                                                                    IKIFQYDQQKNCEEFLNHHNNCSNMQSDINLKDEMLKNKSIECDLLESLNRDQNRLYNKT 125
                                                                                                                                                          VLLYQW-----ILCQGSNYSTCASCPSCPDR----
                                                                                                                                                                                VTYSMVRFHKSAGLQKQVRPEETKGPREAGYRRCSFHWKFIVIALGIFCFLLLVAVSVLA 65
                                                                                         KTVLDSLQHTGRGDKVYWFCYGMKCYYFVMDRKTWSGCKQACQSSSLSLLKIDDEDELKF
                                          LQLVVPSDSCWVGLSYDNKKKDWAWIDNRP---SKLALNTGKYNIRDGGCMLLSKTRLDN
                                                                                                                                                                                                                                                                                    138
167
232
137
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86
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123
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106
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253
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123
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106
1166
223
30498
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21.7%;
                                                                                                                                                                                                                                                                                     MW;
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                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC...) (IN-LINKED (GLCNAC...) (IN-LINKED (GLCNAC...) (IN-LINKED (GLCNAC...) (IN-CE -> KLQ (IN-REF. 2).

A -> T (IN-REF. 2).
A -> T (IN-REF. 2).
                                                                                                                                                                                                                           Score 162; DB 1;
Pred. No. 2.7e-08;
12; Mismatches 92
                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                              CELL ATTACHMENT SITE.
                                                                                                                                                                                                                                                                                                                                                                                                               C-TYPE LECTIN
                                                                                                                                                                                                                                                                                     3C3328D265F71B5E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                (LONG FORM).
                                                                                                                                                                                                                              92;
                                                                                                                                                                                                                                                   Length
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                                                                                                                                                                                                                                                     262;
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Result
No.
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US-09-113-789-9
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SESULT 1 S-08-722-126A-5 Sequence 5, Application US/087221 Patent No. 6034227 GENERAL INFORMATION: APPLICANT: BECHT, ISTAEL APPLICANT: TAL, Michael APPLICANT: TAL, Michael APPLICANT: TAL, Michael APPLICANT: TAL, Michael TITLE OF INVENTION: FUNCTION NUMBER OF SEQUENCES: 20 CORRESSONDENCE ADDRESS: ADDRESSEE: 419 Seventh Street CITY: Washington STATE: 2004 COUNTRY: UNITED STATES OF A ZIP: 20004 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS SOFTWARE: Patentin Release CURRENT APPLICATION NUMBER: PC-DOS/MS SOFTWARE: PAPLICATION DATA: APPLICATION NUMBER: PCT/US9 FILING DATE: 06-APR-1995 CLASSIFICATION NUMBER: US/08/7 FILING DATE: 06-APR-1995 PRIOR APPLICATION NUMBER: 11 1092 FILING DATE: 08-APR-1994 ATTORNEY/AGENT INFORMATION: NAME: BROWDY, ROGET L. REGISTRATION NUMBER: 25,618 REFERENCE/DOCKET NUMBER: PETLEFTAN: (202) 737-3528 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 188 amino acids TYPE: amino acids TYPE: amino acids TYPE: protein MOLECULE TYPE: protein	28 182 17.8 231 29 182 17.8 231 30 182 17.8 231 31 181 17.7 273 32 181 17.7 273 34 180 17.6 216 35 179.5 17.5 293 37 179.5 17.5 292 38 179.5 17.5 292 39 175.5 17.2 201 41 175.5 17.2 201 41 175.5 17.2 201 42 174 170 199 44 173 16.9 209 45 172 16.8 134
D. D. ECULE ENCODING A MAST ASSOCIATED ANTIGEN (MA N.W., Ste. 300 MERICA #1.0, Version #1.30 22,126A 5/04258 CHT-1A	3 US-09-113-789-6 4 US-08-543-246B-6 4 US-08-543-246B-23 2 US-08-680-494A-6 4 US-09-352-302-6 4 US-08-543-246B-24 US-08-543-246B-24 4 US-08-543-246B-24 4 US-08-543-246B-24 4 US-08-688-342-4 2 US-08-688-342-4 2 US-08-113-788-4 2 US-08-13-788-4 3 US-08-772-440-15 3 US-08-772-440-16 3 US-08-772-440-16 3 US-08-772-440-16
FA)	Sequence 6, Appli sequence 23, Appli Sequence 3, Appli Sequence 3, Appli Sequence 6, Appli Sequence 9, Appli Sequence 14, Appli Sequence 17, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli

Query Match

51.4%;

Score 525.5;

DB 3;

Length 188;

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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: prot
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                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 08-APR-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
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REGISTRATION NUMBER: 25,618
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                  Local Similarity 53.5 tes 100; Conservative
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CQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNOEMS 120
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Pred. No. 6.5e-49;
9; Mismatches 57;
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INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: US,
FILING DATE: 08-OCT-199
CLASSIFICATION: 536
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: PCT/I
FILING DATE: 06-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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             135 LRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPLHGVCKKV 187
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OPERATING SYSTEM:
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 61
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                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                      NAME: BROWDY, Roger L. REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                   Local
                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
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                                                                                    CPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCWIG 134
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                                                          CPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIG
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                                                                                                                     66; Conserv
                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                                                              114 amino acids
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                                                                                                                     Conservative
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                   36.2%;
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                                                                       PECHT=1A
                                                                                                                     Score 370.5; DB 3; Pred. No. 1.5e-32; 8; Mismatches 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                     APPLICANT: Lanier, I
APPLICANT: Phillips
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acid
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CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419, Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: PE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 06-APR-1995 PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 08-APR-1994 ATTORNEY/AGENT INFORMATION:
                                   NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                    135 LRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPLHGVCKKV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 202-737-3528
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STRANDEDNESS: Si
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                 61 LRDIDGWRWEDGPALSLS-ILSNSVVQKCGTIHRCGLHASSCEVALQWICEKV 112
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                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                   1 CPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIG 60
                                                                                                                                                                                                                                                                                                                                                                            CPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCWIG 134
                                                                                                                                                        INFORMATION:
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                                                                                                                                                                                          Application US/08738462
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901 California Avenue
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                                                                                 Chang, Chiwen
Lanier, Lewis L.
Phillips Jr., Joseph H.
PRITION: Purified Mammalian
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                     DNAX Research Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                        36.2%; Score 370.5; DB 5 58.4%; Pred. No. 1.5e-32;
                                                                        Related Reagents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Release #1.0, Version #1.30
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PCT-US94-07587-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintos
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ADDRESSEE: Schering Corp.
STREET: One Giralda Farms
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NAME: Ching, Edwin P.
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                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                          APPLICANT:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                         170 GSFLNSNDLEIRGDAKENSCISISQTSVYSEYCSTEIRWICQK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 GSPLNFS--RISSNSFVQTCGAINKNGLQASSCEVPLHGVCKK 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 VEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSE--AFCWIGLR---NNSGWRWED 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 LLTAVLLSVLLYQWILCQGSNYSTCA-----SCPSCPDRWMKYGNHCYYFS 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                        COUNTRY:
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: New Jersey
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                                                                                                                            USA
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                                                                                                                                                                                                                                                                                        Schering
               SYSTEM: Macintosh 7
Microsoft Word 5.1a
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PURIFIED MAMMALIAN NK ANTIGENS AND
                                                                                                                                                                                                                                                        RELATED REAGENTS
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Pred. No. 6.2e-14;
6; Mismatches 81;
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Best Local Similarity
Matches 58; Conserv
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                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: Filed Herewit
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,74
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NO NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                               ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         minc aminc acid TOPOLOGY: 14-
                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 GSPLNFS--RISSNSFVQTCGAINKNGLQASSCEVPLHGVCKK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 HTVNPWNNSLADCSTKESSLLLIRDKDELIHTQNLIRDKAILFWIGLNFSLSEKNWKWIN 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           170 GSFLNSNDLEIRGDAKENSCISISQTSVYSEYCSTEIRWICQK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Lunn, Paul G.
REGISTRATION NUMBER: 32
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91 VEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSE--AFCWIGLR---NNSGWRWED 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                              STREET: 31/4 FV.
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 VVTGLSVSVT----SLIQKSSIEKCSVDIQQSRNKTTERPGLLNCPIYWQQLREKCLLFS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       $
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                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
TELEPHONE: 415 CT. TELEPHONE: 415-845-4166
                                                                                                                                                                                                                                                   MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MTDSVIYSMLELPTATQAQNDYGPQQKSSSSKP-----
                                                                                                                                                                                                                                                                                      94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          225 amino acids
                                                                                                                                                                                                                                                                                                                                                        3174 Porter Drive
                                                                                                                                                                                                                                                                                                      U.S.
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Au-Young, Janice
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                                                                                                                                                                                                                                                                                                                                                                          Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                   Diskette
                                                                                                                                          Filed Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.6%; Score 201; DB 5; 26.0%; Pred. No. 6.2e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                              NOVEL HUMAN MACROPHAGE ANTIGEN
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                                                                                  36,749
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                                                                         PF-0110 US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 5811284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                            TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 179 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1098617
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                                                                                                                                                                                       CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/650,57
                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: :
CORRESPONDENCE ADDRESS:
                                                                                             REFERENCE/DOCKET NUMBER: DX
                                                                                                                                                      FILING DATE: 29-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150 NFSRISSNSF----VQTCGAINKNG-LQASSCEVPLHGVCKK 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 CSCLVAITLGLLTAVLLSVLLYQWILCQGSN--YSTCASCPSCPDRWMKYGNHCYYFSVE 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 CLSLMA-TLGILLKNSFTKLSIEPAFTPGPNIELQKDSDCCSCQEKWVGYRCNCYFISSE 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                           NAME: Ching, Edwin P. REGISTRATION NUMBER:
                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                TELEPHONE:
             ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        94304-1104
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                        California
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Lopez-Botet, Miguel
Phillips Jr., Joseph
Lanier, Lewis L.
                                                                                                                                                                                                                                                                                                                                                                                                                                      901 California Avenue
                                                                  415-496-1200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Purified Mammalian NK Antigens and
                                                                                                                                                                                         us 08/175,339
                                                                                                                                                                                                                                                            US/08/650,578
                                                                                                                           34,090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Joseph H.
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Pred. No. 1.4e-13;
                                                                                                                 DX0391
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// MOLECULE TYPE: protein
US-08-650-578-2
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Patent No. 5
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Best Local Similarity
Matches 53; Conserv
                                                    Matches
                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOSTWARE: FASTSEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/688,3
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                    TELEFAX: 415-845-4166 INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                   IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1098616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS: LENGTH: 179 amino acid
                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150 NFSRISSNSF----VQTCGAINKNG-LQASSCEVPLHGVCKK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 EKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCWIGL---RNNSGWRWEDGSPL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79 QKTWNESRHLCASQKSSLLQLQNTDELDFMS--SSQQFYWIGLSYSEEHTAWLWENGSAL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 CLSLMA-TLGILLKNSFTKLSIEPAFTPGPNIELQKDSDCCSCQEKWVGYRCNCYFISSE 78
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35_CSCLVAITLGLLTAVLLSVLLSVMILCQGSN--YSTCASCPSCPDRWMKYGNHCYYFSVE 92
                                                                     Local
                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                       Similarity
                                                                                                                                                                                                                                                               amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Incyte Pharmaceuticals, Inc
3174 Porter Drive
                                                                                                                                                                                                                                                                               179 amino acids
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                                                    Conservative
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                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                              single
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                                                                     19.2%;
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                                             ; Score 196.5; Ub ...
bred. No. 1.4e-13;
chas 69;
                                                                                                                                                                                                                                                                                                                                                                                           PF-0095-1 CIP
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Pred. No. 1.4e-13;
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                                                                                     Length 179;
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                                                      Gaps
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; MOLECULE TYPE: Pel
; IMMEDIATE SOURCE:
; LIBRARY: GenBanh
; CLONE: 1098616
US-09-113-788-3
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                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compat
OPERATING SYSTEM: DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 31.
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137 -- SQYLFPSFETFNTKNCIAYNPNGNALDESCEDKNRYICKQ 176
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 150 NFSRISSNSF----VQTCGAINKNG-LQASSCEVPLHGVCKK 186
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                                                                    93 EKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCWIGL---RNNSGWRWEDGSPL 149
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                                79 OKTWNESRHLCASOKSSLLOLONTDELDFMS--SSQQFYWIGLSYSEEHTAWLWENGSAL 136
                                                                                                                                      35 CSCLVAITLGLLTAVLLSVLLYQWILCQGSN--YSTCASCPSCPDRWMKYGNHCYYFSVE 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
                                                                                                       20 CLSLMA-TLGILLKNSFTKLSIEPAFTPGPNIELQKDSDCCSCQEKWVGYRCNCYFISSE
                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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3174 Porter Drive
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Pred. No. 1.4e-13;
                                                                                                                                                                             Mismatches
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                                    RESULT 12
PCT-US93-10418-4
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Best Local S
Sequence 4, Application PC/TUS9310418 GENERAL INFORMATION:
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version 1.5
CURRENT APPLICATION DATA:
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LIBRARY: GenBank
CLONE: 1098617
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                                                                                                                                  150 NFSRISSNSF----VQTCGAINKNG-LQASSCEVPLHGVCKK 186
                                                                                                   137 -- SQYLFPSFETFNTKNCIAYNPNGNALDESCEDKNRYICKQ 176
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                                                                                                                                                                                                                                                                                                       Local Similarity
nes 53; Conserv
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STRANDEDNESS: si
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                                                                                                                                                                     QKTWNESRHLCASQKSSLLQLQNTDELDFMS--SSQQFYWIGLSYSEEHTAWLWENGSAL 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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; TOPOLOGY: linear; MOLECULE TYPE: protein PCT-US93-10418-4
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US-09-055-095-4
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Best Local Similarity
Watches 52; Conserv
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                                                                                                                                                                                                             GENERAL INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10418
FILING DATE:
CILECTET PCT/US93/10418
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MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
                                                                                                                                                 APPLICANT: Tang, ....APPLICANT: Patterson, Chandra Corley, Nell C.
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STREET: 31. CITY: Palo Alto
                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                        APPLICANT:
                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                     TITLE OF INVENTION: HUMAN OXIDIZED LDL RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                        176 CEVPLHGVCKK 186
                                                                                                                                                                                                                                                                                                                                                                                                         130 TFLKRYSGELEHWIGLKNEANQTWKWANGKEFNSWFNLTGSG----RCVSVNHKNVTAVD 185
                                                                                                                                                                                                                                                                                                                                                                                                                                        120 SLLQVFLSEAFCWIGLRN--NSGWRWEDGSPLN--FSRISSNSFVQTCGAINKNGLQASS 175
                                                                                                                                                                                                                                                                                                                                       186 CEANFHWVCSK 196
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ADDRESSEE: 11cy...
STREET: 3174 Porter Dr.
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Hjerrild, Kathryn
                                                                                                                                    Corley, Neil
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                                                                Incyte Pharmaceuticals, Inc
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27.2%; Pred. No. 1.6e-13;
tive 27; Mismatches 79
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COMPUTER READABLE FORM: MEDIUM TYPE: Diskett

Diskette

IBM

Compatible

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Best Local :
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           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LIBRARY: GenBank
CLONE: 1902982
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                                                                                                                                                                                                                                     TITLE OF INVENTION:
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LENGTH: 270 amino acid
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ATTORNEY/AGENT INFORMATION
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/0:
FILING DATE: Filed Herewith
                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                   239 CAYIORGTVFAENCILTAFSICOK 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 DELEFIQQMIAHSSFPFWMGLSMRKPNYSWLWEDGTPLTPHLFRIQGAVSRMYPSG---T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 QEMSLLQVFLSEAF -- CWIGL -- - RNNSGWRWEDGSPLN -- -- -- FSRISSNSFVQT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 CGAINKNGLQASSCEVPLHGVCKK 186
                                                                                         COUNTRY: USA
ZIP: 10016-2391
                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 QWILCQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDN 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QEVLKEAANYS-----GPCPQDWLWHEENCYQFSSGSFNWEKSQENCLSLDAHLLKINST 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44;
                                                                                                                                             New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                            261 Madison Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 270 amino acids
                                                                                                                                                                                                                                                                      Masaki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                     Sawamura, Tatsuya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                             McAulay Fisher Nissen Goldberg & Kiel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.9%;
                                                                                                                                                                                                                                   Receptor
                                                                                                                                                                                                                                                Modified Low-Density Lipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        us/09/055,095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 193; Db 4, pred. No. 5.7e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF-0500 US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09352302 Patent No. 6197937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 212 818-9479 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                COMPUTER FADDALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6
FILING DATE: 30-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Sawamura APPLICANT: Masaki,
                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: JG
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 31-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Goldberg, Jules E
REGISTRATION NUMBER: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163 CGAINKNGLQASSCEVPLHGVCKK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 DELEFIQQMIAHSSFPFWMGLSMRKPNYSWLWEDGTPLTPHLFRIQGAVSRMYPSG---T 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 QEVLKEAANYS-----GPCPQDWLWHEENCYQFSSGSFNWEKSQENCLSLDAHLLKINST 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 270 amino acids
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TELEPHONE: 212 818-9479
TELEPHONE: 212 818-9479
                                                                                            CLASSIFICATION:
                                                                                                         APPLICATION NUMBER: US/0 FILING DATE: 12-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 24-MAR
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QEMSLLQVFLSEAF -- CWIGL --- RNNSGWRWEDGSPLN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QWILCQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDN 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44;
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                                                                                                                                                                                                                                                           10016-2391
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                                                                                                                                                                                                                                                                          USA
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                                                                                                                                                                                                                                                                                                                                              McAulay Fisher Nissen Goldberg & Kiel
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24-MAR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.9%; Score 193; DB 2; 30.6%; Pred. No. 5.7e-13; tive 25; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                   Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                  Modified Low-Density Lipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tatsuya
                                                    JP 6-321705
JP 7-214206
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                                                                                                                            US/09/352,302
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5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----FSRISSNSFVQT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
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FILING DATE: 31-JUL-1995

ATTORNEY/AGENT INFORMATION:
NAME: GOIDBER; Jules E
REGISTRATION NUMBER: 24408
REFERENCE/DOCKET NUMBER: JG-YY-4363PCT/D
TELEPHONE: 212 986-4090
TELEPHONE: 212 986-4090
TELEPAX: 212 818-9479
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 270 amino acids
TYPE: aming acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-352-302-2
                                                                                                                                                                      Qγ
Search completed: September 9, 2002, 15:00:04 Job time: 1123 sec
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                                                                                                                                                                                                                                                                   Query Match 18.9%; Score 193; DB 4; Length 270; Best Local Similarity 30.6%; Pred. No. 5.7e-13; Matches 44; Conservative 25; Mismatches 53; Indels
                                                                           22; Gaps
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

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Result
No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB
Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and is derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                     548.5
525.5
525.5
525.5
431
370.5
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                                                                                                                                                                                                                                 1023
1023
789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A_Geneseq_032802:*
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1C23
1 MTDSVIYSMLELPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT:*

| SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
| SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
| SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1992.DAT:*
| SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:*
| SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:*
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| SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
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/SIDS1/gcgdata/hold-geneseqy-geneseqp-embl/AA1981.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1984.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /SIDS1,
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/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1987.DAT:*
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/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000
/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001
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                                                    AAW88277
AAE11761
AAW88267
AAR77472
AAW88266
AAM88815
                                                                                                                                                                      AAE11760
AAR77033
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AAE11759
ABG05451
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                     Rat mast cell func
Rat mast cell func
Human MAFA splice
Partial sequence o
Human MAFA splice
                                                                                                                                                                   Human mast cell fu
Human mast cell fu
Novel human diagno
Mouse mast cell fu
Mammalian mast cel
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Low density Lipopr	AAR99588	17	273	17.7	œ
Type II integral m	AAW4 0219	19	231	7.	182
NKG2 transmembrane	AAR28121	13	215	17.9	183
Type II integral m	AAW40220	19	215	8	184
Primate DCMP2 C-le	AAW88125	20	316	8	185.5
rfa	AAY94345	21	325		Ф
	AAY72948	22	238	8	187.5
n no	AAU19657	22	265		190
Type II integral m	AAW40221	19	233	8	190
NKG2 transmembrane	AAR28118	13	233	ω.	191
~	AAY24153	20	445	8	193
Low density lipopr	AAR99587	17	273	8	193
Bovine LOX-1 polyp	AAB85870	22	270	18.9	193
ч	AAY24152	20	270	œ	193
Low density lipopr	AAR99586	17	270	18.9	193
Chicken 17.5.3 pro	AAW85594	20	257	8	193
O. cuniculus LOX-1	AAB85871	22	278	9.	95
Mouse CD69. Mus m	AAW85595	20	199	9	196.5
e CD69.	AAR54660	15	199	9.	96
O	AAW40222	19	179	9	96
~	AAW64791.	19	179	9	96
Murine mOCILrP1.	AAB68584	22	218	9	197
l anti	AAR65189	16	225	9	201
νoα	AAU19660	22	182	21.2	216.5
e #610	AAM01928	22	. 35	۲.	217
e #639	AAM26602	22	35	21.2	217
Peptide #626 encod	AAM14192	22	35	۲	217
Human bone marrow	AAM66323	22	35	Ľ	217
	AAM53935	22	35	21.2	217
n #603	ABB18604	22	35	۳.	217
Peptide #645 encod	ABB33139	22	35	٠	217
Human peptide #618	ABB27967	22	35	21.2	217
novel extra	AAU19659	22	203	Ñ	226
Human novel extrac	AAU19820	22	198	22.1	226

## ALIGNMENTS

RESULT AAW88265

Human mast cell function-associated antigen (MAFA).

29-MAR-1999 (first entry)

AAW88265

AAW88265 standard; Protein; 189

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29-MAY-1998;
                      03-DEC-1998
                                     WO9854209-A2
                                                                                          Modified-site
                                                                                                                                              Homo sapiens
                                                                                                                                                                     Mast cell function-associated antigen; MAFA; splice variant; human; inflammation; allergy; asthma; rheumatoid arthritis; tumour;
                                                                                                         Modified-site
                                                                                                                        Modified-site
       98WO-GB01572
                                                           /note=
7..10
                                                                                                         /note= "Asn is N-glycosylated" 97..99
                                                                          /note= "/
150..152
                                                                                                                        Location/Qualifiers 65..67
                                                                                          /note= "Asn is N-glycosylated"
137..139
                                                   /note= "ITIM motif"
                                                                                 "Asn is N-glycosylated"
                                                                   "Asn is N-glycosylated"
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RESULTS
AAE11759
ID AAE1
XX AAE1
AC AAE1
XX AAE1
XX AAE1
XX AAE1
XX Huma
XX Huma
XX Huma
XX Huma
XX Imm
OS Homc
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XX Homc
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is the amino acid sequence of human mast cell function-associated antigen (MAPA), a type II membrane glycoprotein. CDNA (see AAV84198) encoding human MAPA can be obtained from myelogenous leukaemic cell line KU812 or cDNA derived from human lung tissue. The encoded protein is similar to the rat form (see AAV8877) having an intracellular domain containing a putative immunoreceptor tyrosine activation motif (ITIM) and an extracellular lectin-like domain. 2 Alternatively spliced forms (see AAV8826-67) of human MAPA have been identified. Polypeptides and synthetic peptides (see AAV88256-64) based on these truncated MAPA proteins can be used in methods for the treatment of inflammatory and allergic diseases,
                                                                                                                                                                                                              Human; pharmaceutical composition; mast cell function associated antigen;
MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
                                                                                                                                                                                                                                                                                                                                                18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polypeptide having a sequence corresponding to human mast cell function-associated antigen - useful in forming and manufacturing pharmaceutical compositions in the treatment of inflammatory and
                              27-SEP-2001
                                                                               WO200170805-A2
                                                                                                                                                                                                                                                                                         Human mast cell function associated antigen (MAFA) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE11759 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure;
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Similarity 100.0%; Pred. No. 1.9e-98;
89; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diseases, and tumour growth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
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                                                                                                                                                                                                            NK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC The present invention relates to a pharmaceutical composition comprising CC an agent which specifically binds to a mast cell function associated CC antigen (MAFA) ligand on a target cell, and prevents or inhibits natural CC killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA CC ligand and a pharmaceutically acceptable excipient. The invention is CC useful for inhibiting an NK - or a T-cell-expressed cell surface MAFA CC binding to a ligand on a target cell, by contacting the pharmaceutical CC composition in vitro, ex vivo or in vivo by administering the composition CC to the subject, to NK or T-cell or the target cell e.g. tumour cell, in CC an amount sufficient to inhibit cell surface MAFA binding to the ligand CC tumour by stimulating the eytotoxic activity of an NK cell or a cytotoxic CC tumour cell. The agent or the composition is useful for treating a CC tumour cytomathy is also useful for inhibiting an activity of CC tumour cell. The invention is also useful for inhibiting an activity of CC NK cell or a T-cell. The present sequence is human MAFA protein.
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Best Local Similarity
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                                                                           Human; chromosome mapping;
                                                                                                             Novel human diagnostic protein #5442
                                                                                                                                             13-FEB-2002
                                                                                                                                                                             ABG05451;
                                                                                                                                                                                                            ABG05451 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pharmaceutical composition for treating tumor by stimulating cytotoxic activity of natural killer cell or T-cell, comprises an agent that binds to mast cell function-associated antigen ligand on target cell
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                                                                                                                                                                                                                                                                                                          181 HGVCKKVRL 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MTDSVIYSMLELPTATQAQNDYGPQQKSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWIL 60
                                                                                                                                                                                                                                                                                                                                                                                                                     CQGSNYSTCASCPSCPDRWKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNOEMS 120
                                                                                                                                                                                                                                                                                                                                                      2001-611482/70.
DB; AAD18734.
                                                              supplement;
                                                                                                                                                                                                                                                                                         hgvckkvrl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189;
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                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                           189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                            mapping; gene mapping; gene therapy; forensic
medical imaging; diagnostic; genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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WO200175067-A2

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AAE11760
ID AAE1
XX
AC AAE1
XX
DT 18-D
XX
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in disconsisting for consider sequences have applications in the disconsisting for the consideration of the constant of the constan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
                                                                                                                                                   AAE11760 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
Mouse mast cell function associated antigen (MAFA) protein.
                                                   18-DEC-2001
                                                                                                    AAE11760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20; SEQ ID No 35810; 103pp; English
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             665
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                                                                                                                                                                                                                                                                                                                                                                                                                          71
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                                                                                                                                                                                                                                                                            cwiglrnnsgwrwedgsplnfsrntngtiirkrkhlhkn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   843 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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2000US-0649167.
                                                 (first entry)
                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77.1%;
89.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 789; DB 22; Length 843; Pred. No. 3.1e-73;
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from WIPO
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Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pharmaceutical composition for treating tumor by stimulating cytotoxic activity of natural killer cell or \mathbb{T}-cell, comprises an agent that binds to mast cell function-associated antigen ligand on target cell -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 19; 49pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-MAR-2000; 2000US-190716P
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180 qwickkv 186
                                                               181 HGYCKKV 187
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                                                                                                                      lfgeylgqdfywiglrnidgwrweggpalsl-riltnsligrcgaihrnglgassceval
                                                                                                                                                                                                                                                                                                                                                                     madssiystlelpeapqvqdesrwklkavlhrphlsrfamvalglltvilmsllmyqril 60
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Pred. No. 4.8e-49;
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Best Local
                                                                                                                                                                                                                                                                                                                     A soluble form of mast cell function-associated antigen (MAFA) can be produced by recombinant techniques for use in the ligand-screening assay. The ligands that are identified may be used alone or in combination with the MAFA to prevent inflammatory and allergic
                                                                                                                                                                                                                                                                                                                                                                                            Novel DNA encoding a mast cell function-associated antigen (MAFA) useful for screening for ligands of MAFA which are useful for prevention of inflammatory and allergic reactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (RYCU/)
(YEDA )
          AAW88277
                              AAW88277
                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Guthmann MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-APR-1995;
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                                                                                                                                                                                                                                                                                                                 reactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      allergic; prevention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mast cell function-associated antigen; MAFA; soluble; ligand;
identification; screening; inflammation; inflammatory; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR77033;
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                                                                                                                               LLQVFLSEAFCWIGLRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPL 180
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                                                                                                                                                                                                                                          Similarity 53.5
00; Conservative
                              standard;
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                                                                                                                                                                                                                                                                                            188 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94IL-0109257.
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                                                                                                                                                                                                                                                                                                                                                                          54pp; English.
                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             function~associated antigen
                                                                                                                                                                                                                                                    51.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tal M;
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Pred. No. 1.
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                                                                                                                                                                                                                                                     No. 1.2e-46;
                                                                                                                                                                                                                                                             DB 16;
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Best Local
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                                                                                                                                                                                                                                                                               This is the amino acid sequence of rat mast cell function-associated antigen (MARA), a type II membrane glycoprotein found on mast cells and basophils. The invention relates to cloning of the human MAFA molecule (see AAW88265) and to the discovery of splice variants (see AAW88266-67) of human MAFA that are not found in rat. Polypeptides and synthetic peptides (see AAW88258-64) based on human MAFA and human truncated MAFA, and polynucleotides encoding them, can be used in methods for the treatment of inflammatory and allergic diseases (e.g. rheumatoid arthritis and asthma), and tumour growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                  allergic diseases, and tumour growth
                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptide having a sequence corresponding function-associated antigen - useful in forming pharmaceutical compositions in the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAY-1997;
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                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 4; 44pp; English.
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N-PSDB; AAV84222.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hewitt EL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PEPT-) PEPTIDE THERAPEUTICS LTD
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180
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                        181 HGVCKKV
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qwicekv
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                                               lfqeyvgedfywiglrdidgwrwedgpalsls-ilsnsvvqkcgtihrcglhassceval
                                                                                                                                                                                                100;
                                                                                                                                                                                              Similarity 53.5
00; Conservative
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                                                                                                                                                                                                                                                          188
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 186
                        187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               allergy; asthma; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    function-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97GB-0011148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98WO-GB01572
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                                                                                                                                                                                                           51.4%;
53.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lamont A,
                                                                                                                                                                                                29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is N-glycosylated'
                                                                                                                                                                                              Score 525.5; DB 20; Pred. No. 1.2e-46; 9; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antigen (MAFA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Williams
                                                                                                                                                                                                                        DB 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              to human mast cell and manufacturing inflammatory and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a pharmaceutical composition comprising an agent which specifically binds to a mast cell function associated antigen (MAFA) ligand on a target cell, and prevents or inhibits natural killer (NK)- or T-cell-expressed cell surface MAFA from binding to MAFA ligand and a pharmaceutically acceptable excipient. The invention is useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA binding to a ligand on a target cell, by contacting the pharmaceutical composition in vitro, ex vivo or in vivo by administering the composition to the subject, to NK or T-cell or the target cell e.g. tumour cell, in an amount sufficient to inhibit cell surface MAFA binding to the ligand on the target cell. The agent or the composition is useful for treating a tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic T-cell (CTL), where the tumour comprises an NK cell or a cytotoxic Tocell. The invention is also useful for inhibiting an activity of the present sermence is rather than a cytotoxic and the present sermence is rather than activity of the present sermence is rather than a cytotoxic and the present sermence is rather than a cytotoxic and the present sermence is rather than a cytotoxic and the present sermence is rather than a cytotoxic and the present sermence is rather than activity of the present sermence is rather than a cytotoxic and the present sermence is rather than a cytotoxic and the present sermence is rather than a cytotoxic and the present sermence is rather than a cytotoxic and the present sermence is rather than a cytotoxic and the present sermence is rather than a cytotoxic and the present sermence is rather than a cytotoxic and the present sermence is rather than a cytotoxic and the present sermence is rather than a cytotoxic and the present sermence is rather than a cytotoxic and the present sermence is rather than a cytotoxic and the present sermence is rather than a cytotoxic and the present sermence is rather than a cytotoxic and the present sermen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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N-PSDB; AAD18736.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Takahashi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-MAR-2000; 2000US-190716P
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                                                                                                                                                                                              HGYCKKY 187
                                                               madnsiystlelpaaprvqddsrwkvkavlhrpcvsylvmvalglltvilmslllyqrtl
                                                                                                                                                                                                                                                                                                                                                                                                        MTDSVIYSMLELPTATQAQNDYGPQQKSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWIL 60
                                                                                                                                      LLQVFLSEAFCWIGLRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Pred. No. 1.2e-46;
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Best Local (
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   181
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   189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.1%;
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associated antigen (MAFA) splice variant huMAFA(E3/4-), which lacks the C-lectin-like domain of human MAFA (see AAW88265) but retains the intracellular and transmembrane domains as well as the extracellular C-terminal tail. Truncated MAFA polypeptides including huMAFA(E3/4-), and polypuccleotides encoding them, as well as synthetic peptides (see AAW88258-64, AAW88268-72), can be used in compositions for the treatment of inflammatory and allergic diseases (e.g. rheumatoid arthritis and asthma), or tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polypeptide having a sequence corresponding to human mast cell function-associated antigen - useful in forming and manufacturing pharmaceutical compositions in the treatment of inflammatory and allergic diseases, and tumour growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mast cell function-associated antigen; MAFA; huMAFA(E3/4-); splice variant; human; inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.
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                                                                                                                                                                                                                                                                                                                        1 MTDSVIYSMLELPTATQAQNDYGPQQKSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWIL
                                                                   LLQVFLSEAFCWIGLRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPL 180
                                                                                                                                                                                                                   CQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMS 120
                                                                                                                                                                                                                                                                                   \verb|mtdsviysmlelptatgaqndygpqqkssssrpscsclvaialglltavllsvllyqwil|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 431; DB 20;
Pred. No. 3.5e-37;
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issnsfvqtcgaitknglqasscevpl
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AAW88266
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AAR77472
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Best Local
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           Human MAFA splice variant huMAFA(E3-).
                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                      or
                                                                                                                                                                                                                                                                                                                                 A soluble form of mast cell function-associated antigen (MAFA) can be produced by recombinant techniques for use in the ligand-screening assay. The ligands that are identified may be used alone
                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 38; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                  Novel DNA encoding a mast cell function-associated antigen (MAFA) useful for screening for ligands of MAFA which are useful for prevention of inflammatory and allergic reactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Guthmann MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-APR-1995;
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                                  29-MAR-1999
                                                        AAW88266
                                                                               AAW88266 standard; Protein; 70 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         allergic; prevention.
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                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                    LRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPLHGVCKKV 187
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                                                                                                                                                                                                                                                                                      114 AA;
                                                                                                                                                                                                                              Conservative
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                                  (first entry)
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screening; inflammation; inflammatory; allergy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                        36.2%; Score 370.5; DB 1 58.4%; Pred. No. 8.5e-31;
                                                                                                                                                                                                                              18;
                                                                                                                                                                                                                                                                                                                    MAFA to prevent inflammatory and allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      function-associated antigen (MAFA).
                                                                                                                                                                                                                              Mismatches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      associated antigen (MAFA) splice variant huMAFA(E3-). huMAFA(E3-) is a major transcript, not found in rat, but highly expressed in human lung and granulocyte-enriched blood cells. The truncated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polypeptide having a sequence corresponding to human mast cell function-associated antigen - useful in forming and manufacturing pharmaceutical compositions in the treatment of inflammatory and allergic diseases, and tumour growth
                                                           07-NOV-2001
                                                                                                                    AAM88815 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                    suppresses the immune system. These peptides, truncated MAFA polypeptides including huMAFA(E3-), and polynucleotides encoding them, can be used be used in compositions for the treatment of inflammatory and allergic diseases (e.g. rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mast cell function-associated antigen; MAFA; huMAFA(E3-);
splice variant; human; inflammation; allergy; asthma;
                                                                                         AAM88815
                                                                                                                                                                                                                                                                                                                                                                                                                         and asthma), or tumour growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This is the amino acid sequence of human mast cell function-
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                             immune/haematopoietic
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63; Conserv
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                                                                                                                                                                                                                                                                                                                   Conservative
                                                        (first entry)
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                                                                                                                       198
                          antigen
                                                                                                                                                                                                                                                                                                                  Score 306.5; DB 20; Pred. No. 2.1e-24; 1; Mismatches 5;
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                             SEQ ID NO:16408
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Human; immune; haematopoietic;

immune/haematopoietic antigen; cancer;

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2000US-0230437. 2000US-0231243. 2000US-0231244. 2000US-0231414. 2000US-0231414. 2000US-0231414. 2000US-023146. 2000US-0231968. 2000US-023299. 2000US-023299. 2000US-023299. 2000US-0232898. 2000US-0232898. 2000US-0232898. 2000US-0232898. 2000US-0232898. 2000US-0232898. 2000US-023398. 2000US-023398. 2000US-0233401. 2000US-0233403. 2000US-0233401. 2000US-0233063. 2000US-0233064. 2000US-0234274.	2000US-0225268. 2000US-0225447. 2000US-0225447. 2000US-0225757. 2000US-0225758. 2000US-0225759. 2000US-0225681. 2000US-02268681. 2000US-0226868. 2000US-0226868. 2000US-0227182. 2000US-0227182. 2000US-0229344. 2000US-0229344. 2000US-0229344. 2000US-0229344. 2000US-0229344. 2000US-0229345.	2000US-0224514 2000US-0214886 2000US-0215647 2000US-0215680 2000US-0215680 2000US-0217487 2000US-0217487 2000US-0217496 2000US-021963 2000US-022964 2000US-0224518 2000US-0225214 2000US-0225214 2000US-0225214 2000US-0225214 2000US-0225266	gene therapy; vaccine;  3.  A2.  A2.  2001WO-US01354.  2000US-0180628. 2000US-0180628. 2000US-0180664. 2000US-01806350. 2000US-01806350. 2000US-0190076. 2000US-0190076.
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Best Local
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                                                                         Human; secreted extracellular matrix protein; immunomodulatory; Anti-HIV; antianemic; antirheumatic; antisclerotic; cardiant; vascular; cerebroprotective; thrombolytic; antimicrobial; ophthalmic; cytostatic;
                                                                                                                                                                                                  04-DEC-2001
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human immunodeficiency virus; rheumatoid arthritis; multiple sclerosis; cancers; hyperproliferative disorder; breast neoplasm; melanoma; Sezary syndrome; Gaucher's disease; neurological diseases;
                                                                                                                                                                                                                                                                             AAU19820 standard; Protein; 198 AA
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                                                           antialzheimers; immune/autoimmune disease; HIV infection; anaemia;
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cytostatic
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Best Local Similarity
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Human; secreted extracellular matrix protein; immunomodulatory;
Anti-HIV; antianemic; antirheumatic; antisclerotic; cardiant; v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antagonists may also be used to down regulate expression and activity of SP and as diagnostic agents for detecting the presence of SPs in samples. The disorders include for example: immune/autoimmune diseases (e.g. HIV (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis and multiple sclerosis), cancers and hyperproliferative disorders (e.g. melanomas, neoplasms of the breast or liver, Sezzry syndrome and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. For example, disorders associated with decreased expression of SPs. The SP polynucleotide or a vector expressing them may be administered to treat diseases by gene therapy. Antisense molecules may be administered to down regulate expression of SPs by binding with the cells own genes and preventing their expression. The polynucleotides may also be used as DNA probes in diagnostic assays. The SPs may also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to isolated nucleic acid molecules encoding novel human secreted extracellular matrix proteins (SPs). The polynucleotides and proteins are used to prevent, treat a medical
                                                           Human novel
                                                                                                   04-DEC-2001
                                                                                                                                          AAU19659
                                                                                                                                                                             AAU19659 standard; Protein; 203 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arrest, tachycardia and angina), infections caused by bacteria, viruses and fungi and ocular disorders (e.g. corneal infections). Other uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaucher's disease), neurological diseases (e.g. Alzheimer's disease, Parkinson's disease) cardio-/cerebrovascular disorders (e.g. cardiac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    used as antigens to produce antibodies and to identify modulators (agonists and antagonists) of the SPs. The anti-(SP) antibodies and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; SEQ ID No 470; 577pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteins, used in preventing, treating or amelion Alzheimer's and Parkinson's diseases and cancers
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05-JAN-2001;
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                                                         extracellular matrix protein,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 226; DB 2
Pred. No. 2e-15;
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                                                         Seq ID
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                                                           No
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  vascular;
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VOV-

08-NOV

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2000US-0246474. 2000US-0246475. 2000US-0246476. 2000US-0246477. 2000US-0246477. 2000US-0246478.

2000US-0241826 2000US-0244617

08-NOV 08-NOV 08-NOV 17-NOV

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17-NOV-

20-OCT 2000)

29-SEP-2000; 02-OCT-2000; 02-OCT-2000; 02-OCT-2000;

29-SEP-2000 29-SEP-2000

2000US-0236370

02-OCT

13-OCT-2000; 13-OCT-2000;

2000US-0237040. 2000US-0239935. 2000US-0239937.

2000US-0237039

2000US-0240960

27-SEP-2000; 29-SEP-2000; 29-SEP-2000;

21-SEP-2000; 25-SEP-2000; 25-SEP-2000; 26-SEP-2000; 27-SEP-2000;

> 2000US-0234274. 2000US-0234997.

17 NOV17 NOV

2000US-0251030. 2000US-0251988. 2000US-0256719. 2000US-0251479. 2000US-0251856.

2000US-0251868. 2000US-0251869. 2000US-0251989. 2000US-0251990.

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08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 108-SEP-2000; 114-SEP-2000; 114-SEP-2000; 114-SEP-2000; 114-SEP-2000;	14-AUG-2000 14-AUG-2000 14-AUG-2000 14-AUG-2000 14-AUG-2000 14-AUG-2000 14-AUG-2000 22-AUG-2000 22-AUG-2000 22-AUG-2000 22-AUG-2000 23-AUG-2000 23-AUG-2000 30-AUG-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000	31-JAN-2000; 04-FEB-2000; 02-KAR-2000; 16-MAR-2000; 11-MAR-2000; 17-MAR-2000; 17-JUN-2000; 07-JUN-2000; 07-JUN-2000; 07-JUL-2000; 07-JUL-2000; 11	cerebroprotect antialzheimers human immunode cancers; hyper Sezary syndrom Alzheimer's di cardiac arrest wound healing; Homo sapiens. WO200155368-AI 02-AUG-2001. 17-JAN-2001; 2
2000US-0231242. 2000US-0231243. 2000US-0231244. 2000US-0231244. 2000US-0231413. 2000US-0231414. 2000US-0231968. 2000US-023299. 2000US-0232399. 2000US-0232399. 2000US-0232399. 2000US-02323400.	2000US-0225267. 2000US-0225270. 2000US-0225247. 2000US-0225757. 2000US-0225758. 2000US-0225758. 2000US-0225758. 2000US-0226881. 2000US-0226881. 2000US-022688.		cerebroprotective; thrombolytic; antimicrobial; ophthalmic; cytostatic; antialzheimers; immune/autoimmune disease; HIV infection; anaemia; human immunodeficiency virus; rheumatoid arthritis; multiple sclerosis; cancers; hyperproliferative disorder; breast neoplasm; melanoma; Sezary syndrome; Gaucher's disease; neurological diseases; Salzheimer's disease; neurological diseases; Alzheimer's disease; neurological diseases; sardiovascular disorder; cardiac arrest; tachycardia; angina; infection; corneal infections; wound healing; immunogen; gene therapy; antisense; food additive. Homo sapiens.  WO200155368-AI.  02-AUG-2001. 2001WO-US01348.
·			15;
סי אים אים אים אים אים אים אים אים אים אי	ייטיטיסיסיסיסיסיסיסיסיסיסיסיסיסיסיסיסיס	ט ט ט ט ט ט ט ט ט ט ט ט ט ט ט ט ט ט ט	קי אין אין די
17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 01-DEC-2000; 01-DEC-2000; 05-DEC-2000; 05-DEC-2000; 05-DEC-2000; 06-DEC-2000;	08-NOV-2000 08-NOV-2000 08-NOV-2000 08-NOV-2000 08-NOV-2000 08-NOV-2000 08-NOV-2000 17-NOV-2000	02-OCT-2000 02-OCT-2000 02-OCT-2000 02-OCT-2000 02-OCT-2000 13-OCT-2000 20-OCT	14 - SEP - 2000 14 - SEP - 2000 14 - SEP - 2000 21 - SEP - 2000 21 - SEP - 2000 25 - SEP - 2000 26 - SEP - 2000 27 - SEP - 2000 27 - SEP - 2000 29 - SEP - 2000
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                                                                                                                                                                                                                                                                                                                                                                               CC The invention relates to isolated nucleic acid molecules encoding CC novel human secreted extracellular matrix proteins (SPs). The CP polynucleotides and proteins are used to prevent, treat a medical CC condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, CC chickens or sheep. For example, disorders associated with decreased CC expression of SPs. The SP polynucleotide or a vector expressing them may be administered to treat diseases by gene therapy. Antisense molecules CC may be administered to down regulate expression of SPs by binding with CC the cells own genes and preventing their expression. The polynucleotides CC may also be used as DNA probes in diagnostic assays. The SPs may also be used as antiponists of the SPs. The anti-(SP) antibodies and CC (agonists and antagonists) of the SPs. The anti-(SP) antibodies and CC antagonists may also be used to down regulate expression and activity of CC The disorders include for example: immune/autoimmune diseases (e.g. HIV (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis and multiple sclerosis), cancers and hyperproliferative disorders (e.g. and multiple sclerosis), cancers and hyperproliferative disorders (e.g. arkinson's disease) neurological diseases (e.g. Alzheimer's disease, CC and fungi and ocular disorders (e.g. corneal infections). Other uses conclude wound healing, maintenance of organs before transplantation,
 BXSXE
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
                                                               14
17967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid molecules encoding human secreted extracellular matrix proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers -
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11-DEC-2000;
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08-DEC-2000;
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08-DEC-2000;
 01-FEB-2002
                           ABB27967;
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                                                    ABB27967 standard; Peptide;
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                                                                                                                                              LHGVCK 185
                                                                                                                                                                        nyvwiglnftslkmtwtwvdgspid----skiffikgpakenscaaikeskifsetcssv 196
                                                                                                                                                                                       -FCWIGLRNNS---GWRWEDGSPLNFSRISSNSFVQ-----TCGAINKNGLQASSCEVP 179
                                                                                                                                                                                                                                                                              giltltlislillvsqgvllkcqkgscsnatqyedtgdlkvnngtrrnisnkdlcasrsa
                                                                                                                                                                                                                                                                                                         GLLTAVLLSVLLY--QWIL--CQG----------SNYSTCASCPS 74
                                                                                                                                                                                                                                                     -----CPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEA 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; 2000US-0251990.
; 2000US-0254097.
; 2001US-0259678.
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2000US-0251989.
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2000US-0251868.
(first entry)
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                                                                                                                                                                                                                                                                                                                                27; Mismatches
                                                     35 AA
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ABB33139
                                                                                                        RESULT
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid probes for measuring gene expression in a sample derifrom human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes .
ABB33139;
                                                    ABB33139 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not form part of printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a spatially-addressable set of single exon
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21-SEP-2000;
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                                                                                                                                                                                                              64 SNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNS
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2000US-0236359.
2000GB-0024263.
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2000US-0608408
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                                                    Peptide;
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                                                                                                                                                                                                                                                                                              0;
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Pred. No. 1
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1.7e-15;
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04-FEB-2002

(first entry)

Peptide #645 encoded by human foetal liver single exon probe.

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Search completed: September Job time: 1189 sec
                                                                                                                         Query Match 21.2%; Score 217; DB 22; Best Local Similarity 100.0%; Pred. No. 1.7e-15; Matches 35; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                       The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                  Claim 27; SEQ ID NO 25774; 639pp + sequence listing; English
                                                                                                                                                                                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-483447/52.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; foetal liver; gene expression; single exon nucleic acid probe.
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27-SEP-2000;
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                                                                  Hanzel DK,
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2000US-0608408.

2000US-0632366.

2000US-02334687.

2000US-0234687.

2000US-0236359.
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              2002, 14:59:44
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Result
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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   Score.
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Match
    100.0
98.4
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1: sp_archea:*
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Gapop 10.0 , Gapext 0.5
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## ALIGNMENTS

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Qy 1 MTDSVIYSMLELPTATQAQNDYGPQQKSSSKPSCSCLY	Query Match  Best Local Similarity 100.0%; Score 1023;    Matches 189; Conservative 0; Mismatches	DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1. SQ SEQUENCE 189 AA; 21079 MW; 15E042AD40B2				RL Biochim. Biophys. Acta 1399:209-212(1998).	RT "Human MAFA has alternatively spliced variants.";	MEDLINE=98438735; PubMed=9765598;			RN {1}	Mammalia; Eutheria; Primates;	hordata;			MAST CHIL FINCTION-ASSOCIATE	DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence u	01-JUN-1998 (TrEMBLrel.	-	43198 PRELIMINARY; PRT; 189	RESULT 1 043198	
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Craniata; Vertebrata; Catarrhini; Hominidae;

Euteleostomi;

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Mismatches 994; No. 1.

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EMBL; AF097358; AADC37200.1; -.
EMBL; AF097358; AADC3719.1; -.
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01-DEC-2001
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SMART; SM00034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SEQUENCE 189 AA; 21206 MW; FA9023F1523656A8
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Mammalia; Eutheria;
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, an ITIM-containing receptor encoded by
and expressed by basophils and NK cells.
Immunol. 28:0-0(1998).
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=C.B-17 SCID;
MEDLINE-99077194; PubMed-9862378;
MEDLINE-99077194; PubMed-99077194; 
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Matches
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Eukaryota; Metazoa; C
Mammalia; Eutheria; R
NCBI_TaxID=10090;
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              STRAIN=129/SYEVINGER | STRAIN=129/SYEVINGER | STRAINE=21115136; PubMed=11220622; Voehringer D., Kaufmann M., Pircher H.; Voehringer Structure, alternative splicing, "Genomic structure, alternative splicing,"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1998 (TrEMBLrel. 08, C)
01-AUG-1999 (TrEMBLrel. 11, La
01-DEC-2001 (TrEMBLrel. 19, La
MAST CELL FUNCTION-ASSOCIATED
LECTIN_LIKE RECEPTOR G1).
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Mammalia; Eutheria;
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01-DEC-2001 (TremBLrel.
SIMILAR TO KILLER CELL I
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[1]
                                                                                                                SEQUENCE FROM N.A.
STRAIN=129/SVEVTACFBR;
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Rodentia;
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Primates;
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Q64335;
                                                                                                                             Proc. Natl Acad Sci. U.S.A. 92:9397-9401(1995).
EMBL; X97191; CAA65829.1; JOINED.
EMBL; X97192; CAA65829.1; JOINED.
EMBL; X97193; CAA65829.1; JOINED.
EMBL; X97193; CAA65829.1; JOINED.
EMBL; X97195; CAA65829.1; JOINED.
EMBL; X97195; CAA65829.1; JOINED.
EMBL; X97195; CAA65829.1; JOINED.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                    InterPro; IPR001304; lectin_c.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                  another
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-SPRAGUE DAWLEY; TISSUBOCCK Jr P., Guthmann M.D., Submitted (APR-1996) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
                                    PROSITE;
                                                                                                                                                                                                                                                                                                        Guthmann M.D., Tal M., Pecht I.;
"A secretion inhibitory signal transduction molecule on mast cells another C-type lectin.";
                                                                                                                                                                                                                                                                                                                                                                 Guthmann
                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96016176; PubMed=7568140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
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MGD; MGI:1355294; Klrq1.
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EMBL; AF097357; AAD03718.1; -.

EMBL; AJ010751; CAA09342.1; -.

EMBL; AF317727; AAK40082.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                    PS50041;
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       <u>Α</u>
C_TYPE_LECTIN_2; 1.
; 21356 MW; 2CC8032D4D020B15 CRC64;
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M.D., Pecht I.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ databases
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Pred. No. 1.0
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Query Match

51.4%;

Score

525.5;

В

Length 188;

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Q9NZS2
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Best Local Similarity
Matches 58; Conser
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SEQUENCE
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                                                                                                                                                                                                               Pfam; PF00059; lectin_c; SMART; SM00034; CLECT; 1
                                                                                                                                                                                                                                        EMBL; AF175206; AAF37804.1; -. EMBL; AJ305370; CAC29425.1; -. InterPro; IPR001304; lectin_c.
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Semenzato G., Biassoni R., Bottino
"Identification of NKp80, a novel t
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09NZS2; O1-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TREMBLrel. 17, Last annotation update)
LECTIN-LIKE RECEPTOR F1 (ACTIVATING CORECEPTOR NKP80)
KLRF1 OR ML/KLRF1.
                                                                                                                                                                                                                                                                                   Eur. J
                                                                                                                                                                                                                                                                                                                                  MEDLINE=21150889; PubMed=11265639; Vitale M., Falco M., Castriconi R.,
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Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                            human natural killer cells."
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MEDLINE=20135860; PubMed=10671213;
Arne I., Renedo M.,
                                                                                                                                                                                                  PROSITE; PS50041; C_TYPE_LECTIN_2; 1
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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  109
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DQTVLCQSEWLKYQGKCYWFSNEMKSWSDSYVYCLERKSHLLIIHDQLEMAFIQKNLRQL
                                                                            GLLTAVLLSVLLY--QWIL--CQG------
                        -----CPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEA 129
                                                   GILTLTLISLILLVSQGVLLKCQKGSCSNATQYEDTGDLKVNNGTRRNISNKDLCASRSA 108
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31.28;
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9; Mismatches 57;
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                                                                                                         Mismatches
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L triggering
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C., Moretta L.
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Best Local S
Matches 51
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01-JUN-2001
01-DEC-2001
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SMART; SM00034; CLECT; 1.
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01-OCT-2000
01-JUN-2001
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MEDLINE-20135860; PubMed-10671213;
MEDLINE-20135860; Arce I., Renedo M.,
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HOmo sapiens (Human).
Homo sapiens (Human).
Arvota; Metazoa; Chordata; Arvota; Primates;
SEQUENCE FROM N.A. STRAIN-C57BL/6J; T
                                             Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                           Q9D403;
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                                   NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                      181 AA;
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
RECEPTOR F1, SPLICE VARIANT 1 KLRF1-S1.
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                                                                                                       (TrEMBLrel.
                                                                                                                             (TrEMBLrel.
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 TISSUE-TESTIS
                                              Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                      21204 MW;
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33.6%;
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17,
19,
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Pred. No. 7.1e
26; Mismatches
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                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Best Local Similarity
Matches 60; Conserv
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01-NOV-1999 (TrEMBLre
01-NOV-1999 (TrEMBLre
01-JUN-2001 (TrEMBLre
NATURAL KILLER CELL I
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Butt C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashina J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Satok H., Satok K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
MEDLINE-99190498; PubMed-10092077; Lohwasser S., Hande P., Mager D.L., "Cloning of murine NKG2A, B and C: receptors on murine NK cells."; Eur. J. Immunol. 29:755-761(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush
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SMART; SM00034; CLECT; 1.

PROSITE; PS50041; C_TYPE_LECTIN_2; 1.

PROSITE; PS50041; C_TYPE_LECTIN_2; 1.

SEQUENCE 275 AA; 31360 MW; C9792BA25C8B5CC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL; AK016908; BAB30491.1;
HSSP; P23807; 1IXX.
                                                                                    SEQUENCE FROM N.A. STRAIN=C57BL/6;
                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                      Mus musculus (Mouse).
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                                                                                                                                                                                                                     (TrEMBLrel. 12, Created)
(TrEMBLrel. 12, Last sequence update)
(TrEMBLrel. 17, Last annotation updat
LER CELL RECEPTOR NKG2B.
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                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                              264
                                                                                                                                                                                                                                                                                                                                                                                                                               186
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                                                                                                                                                      Chordata;
Rodentia;
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31.6%;
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Pred. No. 4.
                                                                                                                                                     Craniata; Veri
Sciurognathi;
                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                   , Takei
second
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hes 73;
                                                                                                                                                                        Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                           B
                             F.;
family of C-type lectin
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                                                                                                                                                      Muridae;
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                                                                                                                                                      Murinae;
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Fukuda S.,
manaka I.,
Saito R.,
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ACCOCC OCCUPATOR REPORT OCCUPATOR REPORT
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Best Local Similarity 29.1
Matches 54; Conservative
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Best Local Similarity
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01-JUN-1998 (
01-JUN-1998 (
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF021350; AAC40050.1; -. InterFoo; IFR001304; lectin_c. pfam; PF00059; lectin_c; 1. SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              054872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIINE-98180346; PubMed-9521051;
Berg S.F., Dissen E., Westgaard I.H., Fos
Molecular characterization of two genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NATURAL KILLER CELL PROTEIN
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SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eur. J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=F344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NKG2A.
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                                                                                                                                                                                                                                                                                                                                                             NON_TER
                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50041; C_TYPE_LECTIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180
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       103
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MTRTYQARPCTRCPDDWISYSHNCYYISVERKSWNDGLTSCISKNCSLLHIDSEEEQAFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WKEDS-----IFKPKIAEILHDECNCAMMSASGLTADNCTTLHPYLCK 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------LVAITLGLLTAVLL-SVLLYQWILCQGSNY--STCASCPSCPDRWMKYGNH
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                                                         ST---
                                                                                                      PSQEQTRICRDCHCKGFPSPPEKLIAGTLGFISFVLIVAVVVITTVATPYTETKAQINSS 102
                                                                                                                                                     PQQKSSSKPSCSC-----LVAITLGLLTAVLLSVLL-----YQWILCQGSNY
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                                  -CASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLL 122
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                                                                                                                                                                                                                                                                                                                                     231 ĀA; 26335
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27.1%;
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                                                                                                                                                                                                          25;
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Last annotation update)
GROUP 2-A (FRAGMENT).
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                                                                                                                                                                                                    Score 210; DB 11;
Pred. No. 4.3e-15;
5; Mismatches 81;
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Pred. No. 4.2e-15;
3; Mismatches 78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                      Length 231;
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Best Local S
Matches 57
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01-DEC-2001
01-DEC-2001
01-DEC-2001
               SEQUENCE FROM N.A.
MEDLINE-20322487; PubMed=10866118;
MEDLINE-20322487; PubMed=10866118;
LaBonte M.L., Levy D.B., Letvin N.L.;
"Characterization of rhesus monkey CD94/NKG2 family
identification of novel transmembrane-deleted forms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Shum B.P., Flodin L.R., Muir D.G.;

"CD94 and NKG2 Genes in Human and Common Chimpanzee.";

Submitted (FEB-2001) to the EMBL/GenBank/DDBJ database

EMBL; AF350005; AAK83792.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NKG2A.
                                                                                                         Macaca mulatta (Rhesus macaque).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Macaca.
                                                                                                                                                                                 01-OCT-2000
01-OCT-2000
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                                                                                                                                                                                                                       Q9MZK3
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            and D."
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nes 57; Conserv
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                                                                                                                                                                                                                                                                                                                                  SIDNEEEMKFLSIISPSS--WIGVFRNSSHHPWVTINGLAFKHEIKDSDNAELNCAVLQV
                                                                                                                                                                                                                                                                                                                                                VITDNQEMSLLQVFLSEAFCWIGL-RNNSGWRWEDGSPLNFSR--ISSNSFVQTCGAINK 168
                                                                                                                                                                                                                                                                                                                                                                                 TLIQRHNNSSLNTRTQKARHCGHCPEEWITYSNSCYYIGKERRTWEESLLACTSKNSGLL
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                                                                                                                                                                                                                                                                                                         NGLQASSCEVPLHGVCKK 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        VIYSMLELPTATQ -- AQNDYGPQQKSSSSKPSCSCLVAITLGLLTAVLL -- -- SVLLYQW
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                                                                                                                                                                                                                                                                                                                                                                                                         ILCQGSNYST-----CASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLL
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                                                                                                                                                                                                                       PRELIMINARY;
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26231 MW;
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Last sequence update)
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                                                                                                                                                                       Last annotation
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Pred. No. 2.6e-14;
4; Mismatches 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Pan.
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Immunogenetics 51:496-499(2000)

EMBL; AF190937; AAF74533.1; HSSP; P06734; 1HLI.

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RESULT
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Best Local S
Matches 59
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Best Local
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Q12918;
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SMART; SM00034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2;
SEQUENCE 225 AA; 25415 MW; 01BI
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U11276; AAA21605.1; --
HSSP; P05140; ZAFP.
InterPro; IPR001304; lectin_c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-94358407; PubMed-8077657;
Lanier L.L., Chang C., Phillips J.H.;
"Human NKR-PlA: A disulfide-linked hor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001304; lectin_c.
pfam; pF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; pS50041; C.TYPE_LECTIN_2;
SEQUENCE 231 AA; 26107 MW; COD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     superfamily expressed by a subset J. Immunol. 153:2417-2428(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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KNGLQASSCEVPLHGVCK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TEGELF-QVELNLQNPSVNHQGIDQIYDCQGLLPPPEKLTAEVLGIICIVLMATVLKTVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSIDNEEEMKFLTAILPSS--WIGVFRNSSHHPWVTINGLTFKHEIKNSDNAEHNCAMLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LC---QGSNYS----TCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHL
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                                                                       VVTGLSVSVT
                                                                                                                 LLTAVLLSVLLYQWILCQGSNYSTCA-----
                                                                                                                                                        MDQQAIYAELNLPT-----DSGPESSSPSSLPRDVCQGSPWHQFALKLSCAGIILLVL-
                                                                                                                                                                                                    MTDSVIYSMLELPTATQAQNDYGPQQKSSSSKP-
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59; Conser
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26.0%;
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                   Score 201; DB 4
Pred. No. 4.1e-1
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Pred. No. 3.7e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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T lymphocytes
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Best Local S
Matches 57
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01-MAR-2001
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PROSITE;
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                                                                                                                                                                       Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Prim
Cercopithecinae; Macaca
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                                                                                                             Cercopithecinae;
NCBI_TaxID=9544;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LaBonte M.L., Levy D.B., Letvin N.L.; "Characterization of rhesus monkey CD94/NKG2 identification of novel transmembrane-deleted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=20322487; PubMed=10866118
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                                                                                                                                                     Mammalia;
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InterPro; IPR001304; lectin_c.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CSCLVAITLGLLTAVLLSVLLYQWILCQGSN--YSTCASCPSCPDRWMKYGNHCYYFSVE
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                                                                                                                                                                                                                                                                                                                                                                                                                    AL--SQYLFPSFETFKPKNCIAYNSKGNALDESCETKNRYICKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EKTWNESRHFCASQKSSLLQLQNRDE---LQDFMSSSQHFYWIGLSYSEEHTAWLWENGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLSLMA-TLGILLKNSFTKLSVEPAYTPGPNIELQKDSDCCSCHEKWVGYRCNCYFISSE
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57; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS50041; C_TYPE_LECTIN_2;
PS00022; EGF_1; UNKNOWN_1
180 AA; 20735 MW; FAF
                                                                                                                                                 Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel.) (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                 (TrEMBLrel.
                                                                                                                                                                                                                                                                       (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                  Macaca
                                                                                                                                                     Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.6%;
                                                                                                                                                                                                                                   16,
16,
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15,
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Last sequence update \\
Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 200; DB
Pred. No. 4.1e
23; Mismatches
                                                                                                                                                                                                                                                      Last sequence
                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                 Last annotation update)
                                                                                                                                                     Catarrhini;
                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FAFA45610278A897
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No. 4.1e-14;
                n I.I.,
NKG2-C
                                                                                                                                                                                                                                                                                                                  231
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                                                                                                                                                                           Vertebrata;
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                                                                                                                                                     Cercopithecidae;
                mRNAs
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d forms
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                                   T.G
                and
                                                                                                                                                                                                                                                                                                                                                                                                                    177
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                                                                                                                                                                           Euteleostomi;
                novel
                alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
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                                                                                                                                                                                                                                                                                                                                                                                                         В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               splicing of 5' exons in rhesus monkey decidua.";
Immunogenetics 53:69-73(2001).
EMBL; AF294889; AAG34501.1; -.
HSSP; P06734; 1HLI.
InterPro; IPR001304; lectin_c.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                     211 ARGLKSNQCESTVIYHCK 228
                                                                                                                                                168 KNGLQASSCEVPLHGVCK 185
                                                                                                                                                                                                             153 LSIDNEEEMKFLTAILPSS--WIGMFHNSSHHPWVTINGLTFKHEIKNSDNAEHNCAMLH 210
                                                                                                                                                                                                                                                         111 LVITDNQEMSLLQVFLSEAFCWIGLRNNSG---WRWEDGSPLNFSRISSNSFVQTCGAIN 167
                                                                                                                                                                                                                                                                                                       93 LIPFPEQSNSSLNTRTQKVRHCGHCPEEWITYSNSCYYIGKEKRTWAESLLACTSKNSSL 152
                                                                                                                                                                                                                                                                                                                                                                                               60 LC---QGSNYS-----TCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHL 110
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